

; PRIOR APPLICATION NUMBER: US 08/244,924
 ; PRIOR FILING DATE: 1994-11-23
 ; PRIOR APPLICATION NUMBER: US 08/278,644
 ; PRIOR FILING DATE: 1994-07-21
 ; NUMBER OF SEQ ID NOS: 30
 ; SOFTWARE: FASTSEQ for Windows Version 4.0
 ; SEQ ID NO 20
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: p53, 321-330
 ; US-08-452-843A-20

Query Match 57.9% Score 4; DB 9; Length 10;
 Best Local Similarity 100.0%; Pred. No. 47;
 Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 3 EYF 6
 DB 6 EYF 9

RESULT 3
 US-10-020-436A-5

; Sequence 5, Application US/10020436A
 ; Patent No. US2002015503A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CLARK, JONATHAN
 ; APPLICANT: LAMONT, ALAN
 ; APPLICANT: WILLIAMS, DAVID
 ; TITLE OF INVENTION: A METHOD FOR MAPPING THE ACTIVE SITES BOUND BY ENZYMES
 ; FILE REFERENCE: 179-54
 ; CURRENT APPLICATION NUMBER: US/10-020-436A
 ; PRIOR APPLICATION NUMBER: 08/244,924
 ; PRIOR FILING DATE: 2002-05-16
 ; PRIOR FILING DATE: 2000-07-26
 ; PRIOR APPLICATION NUMBER: 08/278,644
 ; PRIOR FILING DATE: 1994-10-30
 ; PRIOR APPLICATION NUMBER: GB 9722818.3
 ; PRIOR FILING DATE: 1997-10-30
 ; NUMBER OF SEQ ID NOS: 19
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 5
 ; LENGTH: 5
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
 ; US-10-020-436A-5

Query Match 42.9% Score 3; DB 9; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.7e+05;
 Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 3 EYF 5
 DB 3 EYF 5

RESULT 4
 US-10-020-436A-14

; Sequence 14, Application US/10020436A
 ; Patent No. US2002015503A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CLARK, JONATHAN
 ; APPLICANT: LAMONT, ALAN
 ; APPLICANT: WILLIAMS, DAVID
 ; TITLE OF INVENTION: A METHOD FOR MAPPING THE ACTIVE SITES BOUND BY ENZYMES
 ; FILE REFERENCE: 179-54
 ; CURRENT APPLICATION NUMBER: US/10-020-436A

; CURRENT FILING DATE: 2002-05-16
 ; PRIOR APPLICATION NUMBER: 08/230,431
 ; PRIOR FILING DATE: 2000-07-26
 ; PRIOR APPLICATION NUMBER: PTL 0146, 00019
 ; PRIOR FILING DATE: 1998-10-30
 ; PRIOR APPLICATION NUMBER: GB 9722818.3
 ; PRIOR FILING DATE: 1997-10-30
 ; NUMBER OF SEQ ID NOS: 19
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 14
 ; LENGTH: 5
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
 ; US-10-020-436A-14

Query Match 42.9% Score 3; DB 9; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.7e+05;
 Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 3 EYF 5
 DB 3 EYF 5

RESULT 5

; US-09-911-129B-13
 ; Sequence 13, Application US/090411129B
 ; Publication No. US20030040600A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cleveland State University
 ; APPLICANT: Kalafatis, Michael
 ; APPLICANT: Mann, Kenneth G.
 ; TITLE OF INVENTION: TUBULIN G-ACETYLATION INHIBITOR
 ; FILE REFERENCE: 27433/04004
 ; CURRENT APPLICATION NUMBER: US 09/011129B
 ; CURRENT FILING DATE: 2002-03-13
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 13
 ; LENGTH: 5
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-911-129B-13

Query Match 42.9% Score 3; DB 9; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.7e+05;
 Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 3 EYF 5
 DB 1 EYF 4

RESULT 6

; US-09-859-214-42
 ; Sequence 42, Application US/09850214
 ; Patent No. US20020103111A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Schwender, Charles F.
 ; APPLICANT: Shroff, Hitesh N.

; TITLE OF INVENTION: INHIBITORS OF MACCAM-1-MEDIATED
 ; INTERACTIONS AND METHODS OF USE THEREOF
 ; NUMBER OF SEQUENCES: 89
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
 ; STREET: Two Militia Drive
 ; CITY: Lexington
 ; STATE: Massachusetts
 ; COUNTRY: USA
 ; ZIP: 02421
 ; COMMENTS AVAILABLE FROM:

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: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Ver. 2.0
: CURRENT APPLICATION DATA:
:   APPLICATION NUMBER: US/09/859,214
:   FILING DATE: 16-May-2001
:   CLASSIFICATION: <Unknown>
:   PRIOR APPLICATION DATA:
:     APPLICATION NUMBER: US 09/109,879
:     FILING DATE: 04-JAN-1996
:     APPLICATION NUMBER: US 08/582,740
:     FILING DATE: 04-JAN-1996
:   ATTORNEY/AGENT INFORMATION:
:     NAME: BROOK, David E.
:     REGISTRATION NUMBER: 22,592
:     REFERENCE/DOCKET NUMBER: LKS95-12A2
:     TELEPHONE: (781) 861-6240
:     TELEFAX: (781) 861-9540
:   INFORMATION FOR SEQ ID NO: 42:
:     SEQUENCE CHARACTERISTICS:
:       LENGTH: 5 amino acids
:       TYPE: amino acid
:       STRANDEDNESS: <Unknown>
:       TOPOLOGY: linear
:     MOLECULE TYPE: peptide
:     FEATURE:
:       NAME/KEY: Modified-site
:       LOCATION: 1
:       OTHER INFORMATION: /label= modified aa
:       /note= "Ac - Leucine"
:     FEATURE:
:       NAME/KEY: Modified-site
:       LOCATION: 5
:       OTHER INFORMATION: /label= modified aa
:       /note= "Leucine - NH2"
:     SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-09-959-214-42

Query Match          42.9%  Score 3:  DB 10:  Length 5:
Best Local Similarity 100.0%  Pred No. 2.7e+05:
Matches 3:  Conservative 0:  Mismatches 0:  Indels 0:

QY  5 FTS 7
    |||
DB  2 FTS 4

RESULT 7
US-10-006-630-2
: Sequence 2: Application US/10006630
: Patent No. US20020150926A1
: GENERAL INFORMATION:
:   APPLICANT: Jindal, Satish
:   APPLICANT: Reznier, Fred
:   APPLICANT: Evans, David
:   APPLICANT: Williams, Kevin
:   APPLICANT: Attyan, R.
:   APPLICANT: Fallwal, Sandeep
:   APPLICANT: Pingali, Aruna
:   TITLE OF INVENTION: High Speed, automated, continuous flow, multi-dimensional molecular selection and analysis
:   FILE REFERENCE: SVP-10UDV
:   CURRENT APPLICATION NUMBER: US 10-006,630
:   CURRENT FILING DATE: 2001-12-05
:   PRIOR APPLICATION NUMBER: 09/267,933
:   PRIOR FILING DATE: 1999-03-12
:   PRIOR APPLICATION NUMBER: 60/000,518
:   PRIOR FILING DATE: 1995-06-26
:   PRIOR APPLICATION NUMBER: 09/670,670
:   PRIOR FILING DATE: 1996-06-26
:   NUMBER OF SEQ ID NOS: 17

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: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 2
: LENGTH: 5
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
:   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
:   OTHER INFORMATION: peptide
US-10-006-630-2

Query Match          42.9%  Score 3:  DB 12:  Length 5:
Best Local Similarity 100.0%  Pred No. 2.7e+05:
Matches 3:  Conservative 0:  Mismatches 0:  Indels 0:

QY  3 FTS 5
    |||
DB  2 FTS 4

RESULT 8
US-09-727-963A-25
: Sequence 25: Application US/0977963A
: Patent No. US20020155106A1
: GENERAL INFORMATION:
:   APPLICANT: V I Technologies, Inc.
:   APPLICANT: Hammond, David J.
:   TITLE OF INVENTION: METHOD FOR IDENTIFYING A LIGAND FOR A TARGET MOLECULE
:   FILE REFERENCE: 15242-505
:   CURRENT APPLICATION NUMBER: US/09/727,963A
:   CURRENT FILING DATE: 2000-12-01
:   PRIOR APPLICATION NUMBER: 08/538,638
:   PRIOR FILING DATE: 1999-12-02
:   NUMBER OF SEQ ID NOS: 99
:   SOFTWARE: PatentIn Ver. 2.1
:   SEQ ID NO 25
:   LENGTH: 6
:   TYPE: PRT
:   ORGANISM: Artificial Sequence
:   FEATURE:
:     OTHER INFORMATION: Description of Artificial Sequence: peptide
:     OTHER INFORMATION: ligand
US-09-727-963A-25

Query Match          42.9%  Score 3:  DB 9:  Length 5:
Best Local Similarity 100.0%  Pred No. 2.7e+05:
Matches 3:  Conservative 0:  Mismatches 0:  Indels 0:

QY  4 FTS 6
    |||
DB  4 FTS 6

RESULT 9
US-09-895-072-31
: Sequence 31: Application US/0985072
: Patent No. US2002025590A1
: GENERAL INFORMATION:
:   APPLICANT: CARFIELD, WILLIAM M
:   TITLE OF INVENTION: METHODS FOR PREPARING HIGHLY PURIFIED/ELATED LIPIDAL HYDROGELS
:   FILE REFERENCE: 2101193SCCHT
:   CURRENT APPLICATION NUMBER: 09/135,835,074
:   CURRENT FILING DATE: 2001-07-02
:   PRIOR APPLICATION NUMBER: 60/153,831
:   PRIOR FILING DATE: 1999-09-14
:   PRIOR APPLICATION NUMBER: 09/535,872
:   PRIOR FILING DATE: 2000-09-10
:   NUMBER OF SEQ ID NOS: 52
:   SOFTWARE: PatentIn version 3.1
:   SEQ ID NO 31
:   LENGTH: 6
:   TYPE: PRT
:   ORGANISM: Bos taurus
US-09-895-072-31

```

```

OTHER INFORMATION: Artificial Peptide
US-09-839-447A-52
Query Match 42.9% Score 3; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.7e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FTS 7
DB 4 FTS 5

RESULT 10
US-09-476-388-6
Sequence 6, Application US/09876388
Patent No. US20020049159A1
GENERAL INFORMATION:
APPLICANT: Bridon, Dominique P.
APPLICANT: L'Archeveque, Benoit
APPLICANT: Ezrin, Alan M.
APPLICANT: Holmes, Gailen L.
APPLICANT: Leblanc, Anouk
APPLICANT: St. Pierre, Serge
TITLE OF INVENTION: LONG LASTING INSULINOMIMETIC PEPTIDES
FILE REFERENCE: 500962001610
CURRENT APPLICATION NUMBER: US-09-074,394
PRIOR FILING DATE: 2001-04-24
PRIOR APPLICATION NUMBER: 09/521,618
PRIOR FILING DATE: 2000-09-05
PRIOR APPLICATION NUMBER: PCT/US00/11563
PRIOR FILING DATE: 2000-05-17
PRIOR APPLICATION NUMBER: 60/159,783
PRIOR FILING DATE: 1999-10-15
PRIOR APPLICATION NUMBER: 60/114,436
PRIOR FILING DATE: 1999-05-17
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patent in Ver. 2.1
SEQ ID NO 6
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: Peptide
US-09-876-388-6

Query Match 42.9% Score 3; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.7e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FTS 7
DB 1 FTS 3

RESULT 11
US-09-839-447A-52
Sequence 52, Application US/09839447A
Patent No. US20020058247A1
GENERAL INFORMATION:
APPLICANT: Sallberg, Matti
TITLE OF INVENTION: SYNTHETIC PEPTIDES THAT BIND TO THE
TITLE OF INVENTION: HEPATITIS B VIRUS CORE AND E ANTIGENS
FILE REFERENCE: TPPEP 020GPI
CURRENT APPLICATION NUMBER: US/09/639,447A
PRIOR FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: 09/556605
PRIOR FILING DATE: 2000-04-21
NUMBER OF SEQ ID NOS: 111
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 52
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:

OTHER INFORMATION: Artificial Peptide
US-09-839-447A-52
Query Match 42.9% Score 3; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.7e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FTS 7
DB 4 FTS 5

RESULT 12
US-09-986-552-31
Sequence 31, Application US/09986552
Patent No. US20020150981A1
GENERAL INFORMATION:
APPLICANT: CANFIELD, William
TITLE OF INVENTION: METHODS FOR FINDING HIGHLY PHOSPHORYLATED PROTEIN HYDROLAS
FILE REFERENCE: 2150890S77DIV
CURRENT APPLICATION NUMBER: US/09/986,552
CURRENT FILING DATE: 2001-11-09
PRIOR APPLICATION NUMBER: 09/635,872
PRIOR FILING DATE: 2000-08-10
PRIOR APPLICATION NUMBER: 60/153,831
PRIOR FILING DATE: 1999-09-14
NUMBER OF SEQ ID NOS: 52
SOFTWARE: Patent in version 3.1
SEQ ID NO 31
LENGTH: 6
TYPE: PRT
ORGANISM: Bos taurus
US-09-986-552-31

Query Match 42.9% Score 3; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.7e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FTS 7
DB 3 FTS 5

RESULT 13
US-10-043-487-439
Sequence 439, Application US/10043487
Patent No. US2003035220A1
GENERAL INFORMATION:
APPLICANT: HYBRIGENICS
APPLICANT: Pierre, LEGRAIN
TITLE OF INVENTION: Protein-protein interactions between Shigella flexneri polypep
TITLE OF INVENTION: mammalian polypeptides
FILE REFERENCE: B4778A
CURRENT APPLICATION NUMBER: US/10/043,487
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 09/261,130
PRIOR FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 561
SOFTWARE: Patent in version 3.1
SEQ ID NO 439
LENGTH: 7
TYPE: PRT
ORGANISM: Shigella flexneri
US-10-043-487-439

Query Match 42.9% Score 3; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.7e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YFT 6
DB 3 YFT 5

```

```

RESULT 14
US-09-056-160B-5
? Sequence 5, Application US-09-056-160B
? Patent No. US2002002315A1
? GENERAL INFORMATION:
? APPLICANT: Baca, Manuel
? APPLICANT: Wells, James A.
? APPLICANT: Presta, Leonard G.
? APPLICANT: Lowman, Henry B.
? APPLICANT: Chen, Yvonne M.
? TITLE OF INVENTION: ANTI-VEGF ANTIHEROIC
? NUMBER OF SEQUENCES: 131
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Genentech, Inc.
? STREET: 1 DNA Way
? CITY: South San Francisco
? STATE: California
? COUNTRY: USA
? ZIP: 94080
? COMPUTER READABLE FORM:
? MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: WinPatIn (Genentech)
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER US-09-056-160B
? FILING DATE: 06-Apr-1998
? CLASSIFICATION: 424
? PRIOR APPLICATION NUMBER: 60/054,856
? FILING DATE: 06-AUG-1997
? ATTORNEY/AGENT INFORMATION:
? NAME: Hasak, Janet E.
? REGISTRATION NUMBER: 28,616
? REFERENCE/DOCKET NUMBER: P1093R2
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 650/225-1896
? TELEFAX: 650/952-9881
? INFORMATION FOR SEQ ID NO: 5:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 7 amino acids
? TYPE: Amino Acid
? TOPOLOGY: Linear
US-09-056-160B-5

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Query Match 42.9%; Score 3; DB 10; Length 7;
Best Local Similarity 100.0%; Pred No 2 7e-05;
Matches 3; Conservative 0; Mismatches 0; Indels 0;

```

```

QY 5 FTS 7
DB 1 FTS 3

```

```

RESULT 15
US-09-056-160B-124
? Sequence 124, Application US/09056160B
? Patent No. US2002002315A1
? GENERAL INFORMATION:
? APPLICANT: Baca, Manuel
? APPLICANT: Wells, James A.
? APPLICANT: Presta, Leonard G.
? APPLICANT: Lowman, Henry B.
? APPLICANT: Chen, Yvonne M.
? TITLE OF INVENTION: ANTI-VEGF ANTIHEROIC
? NUMBER OF SEQUENCES: 131
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Genentech, Inc.
? STREET: 1 DNA Way
? CITY: South San Francisco
? STATE: California
? COUNTRY: USA

```

```

? ZIP: 94080
? COMPUTER READABLE FORM:
? MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: WinPatIn (Genentech)
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER US-09-056-160B
? FILING DATE: 06-Apr-1998
? CLASSIFICATION: 424
? PRIOR APPLICATION NUMBER: 60/054,856
? FILING DATE: 06-AUG-1997
? ATTORNEY/AGENT INFORMATION:
? NAME: Hasak, Janet E.
? REGISTRATION NUMBER: 28,616
? REFERENCE/DOCKET NUMBER: P1093R2
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 650/225-1896
? TELEFAX: 650/952-9881
? INFORMATION FOR SEQ ID NO: 124:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 7 amino acids
? TYPE: Amino Acid
? TOPOLOGY: Linear
US-09-056-160B-124

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Query Match 42.9%; Score 3; DB 10; Length 7;
Best Local Similarity 100.0%; Pred No 2 7e-05;
Matches 3; Conservative 0; Mismatches 0; Indels 0;

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```

QY 5 FTS 7
DB 1 FTS 3

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Search completed: April 29, 2003, 09:55:32
Job time : 15 secs

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GenCore version 5.1.1.FS-4579
Copyright (c) 1993 - 2003 Computer Ltd

QM protein - protein search, using sw model

Run On: April 29, 2003, 08:45:15 ; Search time 20.8417 seconds

(without alignments)
23,072 million cell updates/sec

Title: US-09-647-749a

Perfect score: 5

Sequence: 1 LFSYT 5

Scoring table: OLIGO 60 0 0 Gapex 60 0

Searched: 281224 seqs, 96134422 residues

Hit size: 0

Total number of hits satisfying chosen parameters: 1100

Minimum DB seq length: 0

Maximum DB seq length: 10

Post-processing: listing first 45 summaries

2: Pir2**

3: Pir3**

4: Pir4**

Pred No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3	60.0	9	PT0315	Ig heavy chain CRD
2	3	60.0	9	PT0324	Ig heavy chain CRD
3	4	40.0	4	A37912	Phenol 2-methoxy
4	2	40.0	5	I39964	Ribosomal protein
5	2	40.0	5	I39966	Ribosomal protein
6	2	40.0	5	I39965	Ribosomal protein
7	2	40.0	5	I40460	DNAX like protein
8	2	40.0	5	PT0308	Ig heavy chain CRD
9	2	40.0	5	PT0620	Ig kappa chain VJ1
10	2	40.0	5	PT0610	T-cell receptor be
11	2	40.0	5	PT0870	Phytosulfolin alk
12	2	40.0	6	T11779	Phosphoglycerate
13	2	40.0	6	A31262	Dihydrofolate redu
14	2	40.0	6	B31262	Dihydrofolate redu
15	2	40.0	6	T40764	Neuropeptide Y
16	2	40.0	7	XPYDGP	Galactose oxidase
17	2	40.0	7	IRFG7	Hypothalamic hepta
18	2	40.0	7	A50139	Fatty acid synthas
19	2	40.0	7	JN0859	Peptidyl-dipeptida
20	2	40.0	7	B34819	Insulin 57k chain
21	2	40.0	7	T57282	Hypothetical prot
22	2	40.0	7	I55695	Hypothetical L2 pr
23	2	40.0	8	S11078	Glucose-6-phosphat
24	2	40.0	8	B27867	Homeotic protein U
25	2	40.0	8	A28719	Thymic humoral fac
26	2	40.0	8	A15157	Cytochrome P450 AL
27	2	40.0	8	A59028	MHC class I histoc
28	2	40.0	8	A25836	L-serine ammonia-1
29	2	40.0	9	A61357	Phyllocaerulein

30 2 40.0 9 2 Q24180 fibrinogen beta ch
31 2 40.0 9 2 PT0321 Ig heavy chain CRD
32 2 40.0 9 2 PT0324 Ig heavy chain CRD
33 2 40.0 9 2 PT0299 Ig heavy chain CRD
34 2 40.0 9 2 A60427 macrophage cytotox
35 2 40.0 9 2 S66635 alpha-2-macroglobu
36 2 40.0 9 2 S26509 collagen alpha 2(V
37 2 40.0 9 2 I40416 cytochrome 4 - b
38 2 40.0 9 2 A28524 fructose-bisphosph
39 2 40.0 9 2 PT0443 1-oxoacid OCA-tran
40 2 40.0 9 2 S36850 Ig heavy chain V r
41 2 40.0 9 2 G41946 T-cell receptor ba
42 2 40.0 9 2 PT0942 T-cell receptor ba
43 2 40.0 9 2 S85802 hypothetical prote
44 2 40.0 10 1 KHPG7 gonadotropin - 1
45 2 40.0 10 1 KHSR7 gonadotropin - 2

ALIGNMENTS

RESULT 1

PT0315

Ig heavy chain CRD3 region (clone 6-109) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 30-Sep-1993; sequence_revision 30-Sep-1993; text_change 16-Aug-1996

C:Accession: PT0315

R:Khanada, M.; Wasserman, E.; Felchard, E.A.; Shauer, S.; Caton, A.J.; Bevera, S.

J. Exp. Med. 173, 395-407, 1991

A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity an

A:Reference number: PT0315; MIM: 185912

A:Accession: PT0315

A:Molecule type: DNA

A:Residues: 1-9 <YAN>

A:Experimental source: P lymphocyte

C:Keywords: heterotetramer; immunoglobulin

Query Match: (0.0%); Score 3; DB 2; Length 9;

Best Local Similarity: 100.0%; Pred. No. 2.8e-05;

Matches: 3; Conservative: 0; Mismatches: 0; Indels: 0; Days: 0

QY 1 LES 3

DB 5 LES 7

RESULT 2

PT0324

Ig heavy chain CRD3 region (clone 6-109) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 30-Sep-1993; sequence_revision 30-Sep-1993; text_change 16-Aug-1996

C:Accession: PT0324

R:Khanada, M.; Wasserman, E.; Felchard, E.A.; Shauer, S.; Caton, A.J.; Bevera, S.

J. Exp. Med. 173, 395-407, 1991

A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity an

A:Reference number: PT0324; MIM: 185912

A:Accession: PT0324

A:Molecule type: DNA

A:Residues: 1-9 <YAN>

A:Experimental source: P lymphocyte

C:Keywords: heterotetramer; immunoglobulin

Query Match: (0.0%); Score 3; DB 2; Length 9;

Best Local Similarity: 100.0%; Pred. No. 2.8e-05;

Matches: 3; Conservative: 0; Mismatches: 0; Indels: 0; Days: 0

QY 2 ESY 4

DB 6 ESY 8

RESULT 3

A37912

phenol 2-monooxygenase (EC 1.14.11.7) chain P5 - Pseudomonas sp. (strain CF600) (fragment)
 C:Species: Pseudomonas sp.
 C:Date: 14-Jun-1991 #sequence_revision 14-Jun-1991 #text_change 23-Jun-1993

C:Accession: A37832
 R:Powlowski, J.; Shingler, V.
 J. Bacteriol. 172, 6834-6840, 1990
 A:Title: In vitro analysis of polypeptide requirements of multicomponent phenol hydroxylase
 A:Reference number: A37832; MUID:91072231; PMID:140226
 C:Accession: A37832
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-4 <POW>
 C:Keywords: oxidoreductase

Query Match 40.0%; Score 2; DB 2; Length 4;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YT 4

DB 1 SY 2

RESULT 4

139964

ribosomal protein S4 - Bacillus circulans (fragment)

C:Species: Bacillus circulans

C:Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 19-Jul-1996

C:Accession: 139964

R:Grundy, F.J.; Henkin, T.M.

J. Bacteriol. 174, 6763-6770, 1992

A:Title: Characterization of the Bacillus subtilis rpsD regulatory target site.

A:Reference number: 139964; MUID:93015735; PMID:140226

C:Accession: 139964

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-5 <RES>

A:Cross-references: GB:M99041; NID:q143471

C:Genetics:

A:Gene: rpsD

Query Match 40.0%; Score 2; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YT 5

DB 1 SY 2

RESULT 5

139966

ribosomal protein S4 - Bacillus licheniformis (fragment)

C:Species: Bacillus licheniformis

C:Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 19-Jul-1996

C:Accession: 139966

R:Grundy, F.J.; Henkin, T.M.

J. Bacteriol. 174, 6763-6770, 1992

A:Title: Characterization of the Bacillus subtilis rpsD regulatory target site.

A:Reference number: 139966; MUID:93015735; PMID:140226

C:Accession: 139966

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-5 <RES>

A:Cross-references: GB:M99043; NID:q143475

C:Genetics:

A:Gene: rpsD

Query Match 40.0%; Score 2; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YT 5

DB 1 SY 2

DB 4 YT 5

RESULT 6

139965

ribosomal protein S4 - Bacillus megaterium (fragment)

C:Species: Bacillus megaterium

C:Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 19-Jul-1996

C:Accession: 139965

R:Grundy, F.J.; Henkin, T.M.

J. Bacteriol. 174, 6763-6770, 1992

A:Title: Characterization of the Bacillus subtilis rpsD regulatory target site.

A:Reference number: 139965; MUID:93015735; PMID:140226

C:Accession: 139965

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-5 <RES>

A:Cross-references: GB:M99042; NID:q143473

C:Genetics:

A:Gene: rpsD

Query Match 40.0%; Score 2; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YT 5

DB 4 YT 5

RESULT 7

140469

dhazX-like protein - Bacillus subtilis (fragment)

C:Species: Bacillus subtilis

C:Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 21-Jul-1996

C:Accession: 140469

R:Struck, J.C.; Hartmann, R.K.; Toschka, H.Y.; Erdmann, V.A.

Mol. Gen. Genet. 215, 478-482, 1989

A:Title: Transcription and processing of Bacillus subtilis small cytoplasmic RNA.

A:Reference number: 140469; MUID:89218958; PMID:2468993

C:Accession: 140469

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-5 <RES>

A:Cross-references: EMBL:X14796; NID:q46140; PDB:QAA32902.1; F0104572.4

C:Genetics:

A:Start codon: GTG

Query Match 40.0%; Score 2; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SY 4

DB 2 SY 3

RESULT 8

PT0308

Ig heavy chain CDR3 region (clone 6-88) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 18-Aug-1995

C:Accession: PT0308

R:Yamada, M.; Wasserman, P.; Reichard, R.A.; Shane, S.; Caton, A.J.; Kovara, O.

J. Exp. Med. 173, 395-407, 1991

A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity an

A:Reference number: PT0222; MUID:91108337; PMID:1869102

C:Accession: PT0308

A:Molecule type: DNA

A:Residues: 1-5 <YAM>

A:Experimental source: B lymphocyte

C:Keywords: heterotetramer; immunoglobulin

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Query Match          40.0%; Score 2; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ES 3
   ||
Db 3 ES 4

RESULT 9
JT0520
C:Species: Homo sapiens (man)
C:Date: 23-Oct-1992 #sequence_revision 23-Oct-1992 #text_change 16-Apr-1996
C:Accession: JT0520
R:Anker, R.; Conley, M.F.; Pullak, R.A.
J. Exp. Med. 169, 205-2119, 1989
A:Title: Clonal diversity in the B cell repertoire of patients with X-linked agammaglobulinemia
A:Reference number: JT0511; PMID:84279157; PMID:846547
Accession: JT0520
Molecule type: mRNA
A:Residues: 1-5 <ANK>
A:Note: The sequence shown here is one of eight productive V-D-J mu chain rearrangements
A:Note: A stop codon terminates the sequence in the V region
C:Keywords: heterotetramer; immunoglobulin
F.1-5/Domain V kappa region <VSE>

Query Match          40.0%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ES 3
   ||
Db 2 ES 3

RESULT 10
JT0610
T-cell receptor beta chain V D-J region (100-2E) mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 10-May-1997
C:Accession: JT0610
R:Peeney, A.T.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: JT0509; PMID:41277601; PMID:11559
Accession: JT0610
C:Keywords: translation not shown
Molecule type: mRNA
A:Residues: 1-5 <PEE>
A:Experimental source: newborn thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match          40.0%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ES 3
   ||
Db 4 ES 5

RESULT 11
JT0870
Phytosultokine alpha - garden asparagus (fragment)
C:Species: Asparagus officinalis (garden asparagus)
C:Date: 20-Apr-2002 #sequence_revision 20-Apr-2002 #text_change 19-Apr-2002
C:Accession: JT0870
R:Katsubayashi, Y.; Sakadami, Y.
Proc. Natl. Acad. Sci. U.S.A. 91, 7623-7627, 1994
A:Title: Phytosultokine, a sulfated peptides that induce the proliferation of single mesophyll cells
A:Reference number: JT0870

Query Match          40.0%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ES 3
   ||
Db 4 ES 5

RESULT 12
T11779
Phosphoglycolate transport regulatory protein ptaA - Salmonella typhimurium (fragment)
C:Species: Salmonella typhimurium
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C:Accession: T11779
R:Yang, Y.L.; Goldrick, D.; Hong, J.S.
J. Bacteriol. 170, 4299-4303, 1988
A:Title: Identification of the products and nucleotide sequences of two regulatory genes, ptaA and ptaB, that control phosphoglycolate transport in Salmonella typhimurium
A:Reference number: 217239; PMID:8314933; PMID:2842311
Accession: T11779
A:Status: Preliminary; translated from GB/EMBL/DBJ
Molecule type: DNA
A:Residues: 1-6 <YAN>
A:Cross-references: EMBL:M21279; NID:858752; PMID:8154260
A:Experimental source: strain D12

Query Match          40.0%; Score 2; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LE 2
   ||
Db 2 LE 3

RESULT 13
A31263
Dihydrofolate reductase EC 1.5.1.3, 7-thymidylate synthase (E. coli), Plasmodium falciparum
C:Species: Plasmodium falciparum
C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 20-Mar-1996
C:Accession: A31263
R:Peterson, D.S.; Walliker, D.; Wellem, T.E.
Proc. Natl. Acad. Sci. U.S.A. 95, 9114-9119, 1998
A:Title: Evidence that a point mutation in dihydrofolate reductase-thymidylate synthase confers resistance to pyrimethamine in Plasmodium falciparum
A:Reference number: A94217; PMID:89057886; PMID:2904149
Accession: A31263
A:Status: not compared with conceptual translation
Molecule type: cDNA
A:Residues: 1-6 <PET>
C:Keywords: methyltransferase; NADPH oxidoreductase

Query Match          40.0%; Score 2; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ES 3
   ||
Db 4 ES 5

RESULT 14
B31263
Dihydrofolate reductase-thymidylate synthase (E. coli), Plasmodium falciparum
C:Species: Plasmodium falciparum
C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 20-Mar-1996
Accession: B31263
R:Peterson, D.S.; Walliker, D.; Wellem, T.E.
Proc. Natl. Acad. Sci. U.S.A. 95, 9114-9119, 1998
A:Title: Evidence that a point mutation in dihydrofolate reductase-thymidylate synthase confers resistance to pyrimethamine in Plasmodium falciparum
A:Reference number: A94217; PMID:89057886; PMID:2904149
Accession: B31263
A:Status: not compared with conceptual translation
Molecule type: cDNA
A:Residues: 1-6 <PET>
C:Keywords: methyltransferase; NADPH oxidoreductase

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A:Reference number: A94217; PMID:89057886; PMID:117808

A:Accession: B31263

A:Status: not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-6 <PET>

C:Keywords: methyltransferase; NADP; oxidoreductase

Query Match: 40.0%; Score 2; DB 2; Length 6;

Best Local Similarity 100.0%; Pred No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ES 3

II

Db 4 ES 5

RESULT 15

JH0784

ropeptide TE-6 - pig roundworm (fragment)

Species: Ascaris suum (pig roundworm)

Date: 10-Jun-1993; #sequence_revision 10; #text_change 28-Apr-1995

C:Accession: JH0784

R:Smart, D.; Shaw, C.; Curry, W.J.; Johnston, C.F.; Thim, L.; Halton, D.W.; Buchanan, K.

Biochem. Biophys. Res. Commun. 187, 1323-1329, 1992

A:Title: The primary structure of TE-6: a novel neuropeptide from the nematode Ascaris

A:Reference number: JH0784; PMID:93038603; PMID:117808

A:Accession: JH0784

A:Molecule type: protein

A:Residues: 1-6 <SMA>

A:Experimental source: gonaduct

C:Keywords: neuropeptide

Query Match: 40.0%; Score 2; DB 2; Length 6;

Best Local Similarity 100.0%; Pred No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LE 2

II

Db 5 LE 6

Search completed: April 29, 2003, 08:54:18

Job time : 22.833 secs


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RX NCBI_TaxID=9821;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RX MEDLINE=8121390; PubMed=6263776;
PA Chang P C C., Huang W Y., Arimura A., Redding T W., Coy D. H.,
FA Saifan M., Kong A., Hamilton J. W., Cohen D. V., Schally A. V.,
RT "Isolation, structure and synthesis of a heptapeptide with in vitro
RT ACTH-releasing activity from porcine hypothalamus."
RL Horm. Metab. Res. 13:226-232(1981).
SQ SEQUENCE 7 AA: 957 MW: 632545b1e850c2a0 CRC64;
Query Match 40.0%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SY 4
DB 5 SY 6

RESULT 3
ID IGAO_DACDE STANDARD; PRI: 7 AA.
AC P06294;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE Galactose oxidase inhibitor.
OS Dactylium dendroides (Cladobotryum dendroides).
OC Eukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes;
OC Hypocreales; Hypocreaceae; Hypomyces.
OX NCBI_TaxID=5132;
RN [1]
RP SEQUENCE.
RX Avigad G., Markus Z.;
RT "Identification of a peptide inhibitor of galactose oxidase from
RT Dactylium dendroides."
RL Fed. Proc. 31:447-447(1972).
CC -!- FUNCTION: BINDS ONE COPPER ION PER MOLE OF THE BUT DOES NOT BIND THE
CC GALACTOSE OXIDASE APOENZYME. IT MAY INACTIVATE THE ENZYME BY
CC BINDING TO ITS PROSTHETIC COPPER GROUP
DK PIR: A01341; XEYDGD.
KW Copper, Metalloenzyme inhibitor.
SQ SEQUENCE 7 AA: 706 MW: 75BB01A456D87D80 CRC64;
Query Match 40.0%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 2 ES 3
DB 6 ES 7

RESULT 4
ID ALL6_CARMA STANDARD; PRI: 8 AA.
AC P81819;
DT 30-MAY-2000 (Rel. 19, Created)
DT 30-MAY-2000 (Rel. 19, Last sequence update)
DT 30-MAY-2000 (Rel. 19, Last annotation update)
DE Carcinustatin 16.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota, Metazoa, Arthropoda, Mandibulata, Funiculata, Crustacea;
OC Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata;
OC Brachyura; Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RX TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=96121193; PubMed=9461295;
PA Duve H., Cohnsen A. H., Maestro J.-L., Scott A. G., Jaros P. P.,

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RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas."
RL Eur. J. Biochem. 250:757-764(1997).
CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation; Multigene family.
FT MOD_RES 8 AMIDATION.
SV SEQUENCE 8 AA: 613 MW: 73286545A576878 CRC64;
Query Match 40.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SY 4
DB 5 SY 6

RESULT 5
ID UPAL_HUMAN STANDARD; PRI: 8 AA.
AC P30087;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Unknown protein from CD-page of plasma (Spec 2) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini, Hominiidae, Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX TISSUE=Plasma;
RX MEDLINE=9309293; PubMed=1459097;
PA Hughes G. J., Frutiger S., Faquet N., Rivier F., Pasquali C.,
PA Sanchez J.-C., James P., Tissot J.-D., Bjellqvist B.,
PA Hochstrasser D. F.;
RT "Plasma protein map: an update by microsequencing."
RL Electrophoresis 13:707-714(1992).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 4.9, ITS MW IS: 65 KDA
DR SWISS-2DPAGE; P30087; HUMAN.
FT NON_TER 1
FT UNSURE 8
FT NON_TER 8
SQ SEQUENCE 8 AA: 944 MW: C01772455BB06DA CRC64;
Query Match 40.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ES 3
DB 3 ES 4

RESULT 6
ID FIBB_MACFU STANDARD; PRI: 9 AA.
AC P19345;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Fibrinogen beta chain (Contains: Fibrinopeptide B) (Fragment).
OS FGB.
OS Macaca fuscata fuscata (Japanese macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9543;
RN [1]
RP SEQUENCE.

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RX MEDLINE=85289140; PubMed=3928610;
RA Nakamura S, Takenaka O, Takahashi K;
RT "Fibrinopeptides A and B of Japanese monkey (Macaca fuscata) and
RT pates monkey (Erythrocebus patas): their amino acid sequences,
RT restricted mutations, and a molecular phylogeny for macaques,
RT quonons, and baboons.";
RL J. Biochem. 97:1487-1492(1985);
CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NON-IDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THIS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOLID CLOT.
DR PIR: C24190; C24180.
DR InterPro: IPR002181; Fibrinogen_C.
DR PROSITE: PS00514; FIBRIN_AG_C_DOMAIN: PARTIAL
R Blood coagulation: Plasma.
PEPTIDE 1 9 FIBRINOPEPTIDE B
NON_TER 1 9
SQ SEQUENCE 9 AA: 1038 MW: 69F65B9C735B81P CPC64:
Query Match 40.0% Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 ES 3
DB 3 ES 4
RESULT 7
PGLR_DIAAB
ID PGLR_DIAAB STANDARD: PRT: 9 AA.
AC P81179;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Endo-polygalacturonase (PG) (EC 3.2.1.15) (Fragment).
OS Diaprepes abbreviatus (Superficially parasitic lepidopteran).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Insecta; Lepidoptera;
OC Insecta; Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga
OC Cucujiformia; Phytophaga; Curculionidae; Eurytominae; Eurytomini.
OC Diaprepes
OX NCBI_TaxID=11040;
RN [1]
SEQUENCE.
TISSUE=Larval gut;
RA Doostdar H., McCollum T.G., Mayer R.T.;
RT "Purification and characterization of an endo polygalacturonase from
RT the gut of West Indian sugarcane root borer weevil (Diaprepes
RT abbreviatus L.) larvae.";
RL Comp. Biochem. Physiol. 118B:861-867(1997);
CC -1- CATALYTIC ACTIVITY: Random hydrolysis of 1,4-alpha-D-
CC galactosiduronic linkages in pectate and other galacturonans.
CC -1- INDUCTION: INHIBITED BY CITRUS PGIP.
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN IS:
CC 9.4, ITS MW IS: 44.5 kDa
CC -1- SIMILARITY: WEAK TO OTHER POLYGALACTURONASES.
KW Hydrolase; Glycosidase; Cell wall.
FT NON_TER 9
SQ SEQUENCE 9 AA: 1041 MW: 1F49087042D841P CPC64:
Query Match 40.0% Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 YT 5
DB 2 YT 3

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RESULT 8
UHA2_HUMAN
ID UHA2_HUMAN STANDARD: PRT: 9 AA.
AC P40929;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-OCT-2001 (Rel. 40, Last annotation update)
LE Unknown protein from 2D-page of heart (Spot 5603) (Fragment).
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE.
TISSUE=Heart;
FX MEDLINE=91203297; PubMed=7895722;
RA Corbett J.M., Wheeler C.H., Baker C.S., Yacoub M.H., Dunn M.C.;
RT "The human myocardial two-dimensional gel protein database: update
RT 1994.";
RL Electrophoresis 15:1455-1465(1994);
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKN KN
CC PROTEIN IS: 6.0, ITS MW IS: 55.3 kDa.
FT NON_TER 9
SQ SEQUENCE 9 AA: 1104 MW: 8874B1B85B01B2CA CRC64:
Query Match 40.0% Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 YT 5
DB 6 YT 7
RESULT 9
ULAE_HUMAN
ID ULAE_HUMAN STANDARD: PRT: 9 AA.
AC P31931;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Unknown protein from 2D-page of liver tissue (Spot 110) (Fragment).
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE.
TISSUE=Liver;
RX MEDLINE=94147969; PubMed=8313870;
RA Hughes G.J., Frutiger S., Paquet N., Pasquali C., Sanchez J.-M.,
RA Tissot J.-D., Reibich A., Appel S.B., Hochstrasser D.F.;
RT "Human liver protein map: update 1993.";
LE Electrophoresis 14:1216-1224(1993);
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKN KN
CC PROTEIN IS: 5.5, ITS MW IS: 11 kDa.
DB SWISS-2DPAGE; P31931; HUMAN.
FT NON_TER 9
SQ SEQUENCE 9 AA: 1096 MW: 477B3B173AE729C7 CRC64:
Query Match 40.0% Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LE 2
DB 6 LE 7
RESULT 10
ULAH_HUMAN
ID ULAH_HUMAN STANDARD: PRT: 9 AA.

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AC P31944;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Unknown protein from 2D-page of liver tissue (Fragment).
 OS Homo sapiens (Human).
 QS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Liver;
 RX MEDLINE=94147969; PubMed=8313870;
 RA Hughes G.J., Frutiger S., Paquet N., Pasquali C., Sanchez J.C.,
 KA Tissot J.-D., Bairoch A., Appel R.D., Hochstrasser D.F.,
 RL Human liver protein map: update 1993."
 RL Electrophoresis 14:1216-1222(1993).
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED P.P. OF THIS UNKNOWN
 CC PROTEIN IS 5.5, ITS MW IS: 12 kDa.
 CC SWISS-2DPAGE: P31944; HUMAN.
 CC NON_TER 1
 CC VARIANT 1 3
 CC A - L
 CC /FTID-VAR_000541;
 FT NON_TER 9
 FT SEQUENCE 9 AA: 990 MW: FLOC7B17AB6DLCA CRC64;
 Query Match 40.0%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1,1e+75;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LE 2

DB 6 LE 7

RESULT 11
 ID UN19_CLOPA STANDARD: PRT: 9 AA
 AC P41355;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Unknown protein CP 19 from 2D-page (Fragment).
 OS Clostridium pasteurianum.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae.
 OX Clostridium.
 OX NCBI_TaxID=1501;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=W5;
 RX MEDLINE=98291870; PubMed=9629928;
 RA Flensburg R., Skjeldal L.;
 RT "Two-dimensional gel electrophoresis separation and N-terminal
 RT sequence analysis of proteins from Clostridium pasteurianum W5."
 RL Electrophoresis 19:802-806(1998).
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED P.P. OF THIS UNKNOWN
 CC PROTEIN IS: 6.5, ITS MW IS: 36.0 kDa.
 CC VARIANT 8 9
 CC M -> D.
 FT NON_TER 9
 FT SEQUENCE 9 AA: 1128 MW: E31E9B0AF5BBI9CA CRC64;
 Query Match 40.0%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1,1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ES 3

DB 4 ES 5

RESULT 12

AMPN_HELAM

ID AMPN_HELAM STANDARD: PRT: 10 AA.

AC P81731;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Aminopeptidase N (EC 3.4.11.2) (CytA(C) receptor) (Fragment).
 OS Helicoverpa armigera (Cotton bollworm).
 QS Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata;
 OC Ditrysia; Noctuoidea; Noctuidae; Heliothinae; Helicoverpa.
 OX NCBI_TaxID=29058;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Midgut;
 RA Ingle S.S., Trivedi N., Prasad R., Rao K.K., Chatterji H.S.;
 RT "Aminopeptidase-N as a receptor for Bacillus thuringiensis (CytA)
 RT toxin from Helicoverpa armigera."
 RL Submitted MAAS 1919; to the SKISS-FRONT data bank.
 CC -1- FUNCTION: ACTS AS A PEPTIDE RECEPTOR FOR B. THURINGIENSIS TOXIN (CYT-A).
 CC -1- CATALYTIC ACTIVITY: Release of an N-terminal amino acid.
 CC Preferably a neutral or hydrophobic one, from a poly-peptide.
 CC Aminoacyl-tylamides are poor substrates.
 CC -1- COFACTOR: BINDS AND REQUIRES A ZINC ATOM, WHICH IS ESSENTIAL FOR
 CC PROTEOLYTIC ACTIVITY (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M1.
 DR InterPro: IPR000136; 20_MiPeptidse.
 DR PROSITE: PS00142; ZINC_PROTEASE; PARTIAL.
 KW Hydrolase; Metallopeptase; Aminopeptidase; Zinc.
 FT NON_TER 10
 FT SEQUENCE 10 AA: 1093 MW: 05042EB87B11F1B9 CRC64;
 Query Match 40.0%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 4.3e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YT 5

DB 4 YT 4

RESULT 13

CA12_LITCI

ID CA12_LITCI STANDARD: PRT: 10 AA

AC P82086;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Caerulein 1.2/1.2V4.

OS Litoria citropa (Australian blue mountains tree frog) and

OS Litoria splendida (Magnificent tree frog).

OC Euzaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;

OC Pelodyadinae; Litoria.

OX NCBI_TaxID=94770; 30345;

RN [1]

RP SEQUENCE AND MASS SPECTROMETRY (CAERULEINS 1.2 AND 1.2V4).

RC SPOTTEST citropa; TISSUE=Skin secretion;

FX MEDLINE=20057761; PubMed=10584099;

RA Wabnitz P.A., Bowie J.H., Tyler M.J.;

RT "Caerulein-like peptides from the skin glands of the Australian tree

RT frog Litoria splendida. The discovery of the aquatic male sex

RT pheromone splendipherin, together with Phe8 caerulein and the

RT antibiotic peptide caerin 1.10."

PL Eur. J. Biochem. 267:269-275(2000).

CC -1- FUNCTION: HYPOTENSIVE NEUROPEPTIDE (PROBABLE).

CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
 CC -1- PFM: IS:POPM 1 2Y4 DIFFERS FROM IS:PEM 1 1 IN NAL BEING
 CC SULFATED.
 CC -1- MASS SPECTROMETRY: MW-1356; METHOD=Electro-spray.
 CC -1- SIMILARITY: BELONGS TO THE GASTRIN/CHOLESTYKININ FAMILY
 DR InterPro: IPR001651; Gastrin.
 DR PROSITE: PS00259; Gastrin.
 KW Amphibian skin; Hypotensive agent; Amidation; Sulfation.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 4 4 SULFATION.
 FT MOD_RES 10 10 AMIDATION.
 SQ SEQUENCE 10 AA: 1366 MW: 998562786464.3654;

Query Match 40.0%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 4.3e+03;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 YT 5
 ||
 4 YT 5

RESULT 14

CAER_LITXA STANDARD; PRT: 10 AA.
 AC P56264;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Caerulia.
 CS Litoria xanthomera (Orange-thighed frog).
 CC Eukaryota; Chordata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Neobatrachia; Batrachia; Hylidae;
 CC Pelodyadinae; Litoria.
 OX NCBI_TaxID=79697;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 PC TISSUE=Skin secretion;
 RX MEDLINE=97374000; PubMed=9230483;
 RA Steinborner S T, Waugh P J, Rowie J H, Wallace J C, Tyler M J,
 Ramsay S L;
 RT "New caerin antibacterial peptides from the skin glands of the
 RI Australian tree frog Litoria xanthomera";
 RL J. Pept. Sci. 3:181-185(1997).
 CC -1- FUNCTION: HYPOTENSIVE NEUROPEPTIDE
 CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
 CC -1- MASS SPECTROMETRY: MW-1354; METHOD=FAB.
 CC -1- SIMILARITY: BELONGS TO THE GASTRIN/CHOLESTYKININ FAMILY.
 DR InterPro: IPR001651; Gastrin.
 DR PROSITE: PS00259; Gastrin; 1.

KW Amphibian skin; Hypotensive agent; Amidation; Sulfation.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 4 4 SULFATION.
 FT MOD_RES 10 10 AMIDATION.
 SQ SEQUENCE 10 AA: 1290 MW: 99856337861864 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 4.4e+03;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 YT 5
 ||
 4 YT 5

RESULT 15

GONL_ALLMI STANDARD; PRT: 10 AA.
 AC P37041; P20407.
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-DEC-1996 (Rel. 37, Last annotation update)
 DE Gonadoliberin I (Gonadotropin-releasing hormone I) (GnRH-I) (LH-RH I)

DE (Loltherin I).
 CS Alligator mississippiensis (American alligator).
 CC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 CC Archosauria; Crocodylia; Alligatorinae; Alligator.
 OX NCBI_TaxID=4466;
 RN [1]
 RP SEQUENCE.
 PC TISSUE=Brain;
 RX MEDLINE=9152336; PubMed=1862682;
 RA Lovejoy D.A., Fischer W.H., Fisher G.B., McEwen J.E., Park W.,
 Lance V., Swanson P., Rivier J.E., Sherwood N.M.;
 RT "Primary structure of two forms of gonadotropin-releasing hormone
 from brains of the American alligator (Alligator mississippiensis)".
 RL Regul. Pept. 33:105-116(1991).
 CC -1- FUNCTION: STIMULATES THE SECRETION OF GONADOTROPINS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE GnRH FAMILY.
 DR PIR: A60066; RHAQ1.
 DR InterPro: IPR002012; GnRH.
 DR Pfam: PF00446; GnRH; 1.
 DR PROSITE: PS00473; GnRH; 1.
 KW Hormone; Amidation; Hypothalamus.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 10 10 AMIDATION.
 SQ SEQUENCE 10 AA: 1172 MW: 28482307286845A3 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 4.3e+03;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 SY 4
 ||
 4 SY 5

Search completed: April 29, 2003, 08:52:28
 Job time : 13.6667 secs


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DI 01-FEB-1997 (TrEMBLrel. 02, Created)
DI 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DI 01-FEB-2000 (TrEMBLrel. 12, Last annotation update)
DE Alginatase lyase (Fragment).
GN ALY.
OS Pseudomonas sp. (strain OS-ALG-9).
OC Bacteria; Proteobacteria.
OX NCBI_TaxID=86018;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OS-ALG-9;
RA Fujiyama K.;
RL Submitted (01-1994) to the EMBL/GenBank/TrEMBL databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=OS-ALG-9;
RA Maki H., Mori A., Fujiyama K., Kinoshita S., Yoshida T.,
  "Cloning, sequence analysis and expression of Escherichia coli
  gene encoding an alginatase from Pseudomonas sp. OS-ALG-9."
  J. Gen. Microbiol. 139:987-993(1993)
  EMBL: D38469; HAA21704.1; -.
KW Lyase.
FT NON-TER 1 1
FT NON-TER 8 8
SQ SEQUENCE 8 AA: 841 MW: 461005585B041B AC64:

Query Match 40.0%; Score 2; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YT 5
DB 1 YT 2

RESULT 4
QYRXO
ID QYRXO PRELIMINARY: PRT: 6 AA.
AC QYRXO
DI 01-MAY-2000 (TrEMBLrel. 13, Created)
DI 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DI 01-MAY-1999 (TrEMBLrel. 12, Last annotation update)
DE Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit
  (Fragment).
GN RBL.
OS Bacteria; Cyanobacteria; Oscillatoriales; Rhodospirillaceae.
OX NCBI_TaxID=59512;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BC-PLA 9316, AND BC-PLA 9309;
RX MEDLINE=20005589; PubMed=10537197;
RA Beard S.J., Handley B.A., Hayes P.K., Walsh A.E.;
  "The diversity of gas vesicle genes in Planctothrix rubescens from
  Lake Zurich."
  Microbiology 145:2757-2768(1999).
DR EMBL: AJ132249; CAB59537.1; -.
DR EMBL: AJ132248; CAB59534.1; -.
FT NON-TER 1 1
SQ SEQUENCE 8 AA: 957 MW: 330100055B041B AC64:

Query Match 40.0%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ES 3
DB 3 ES 4

RESULT 4
QYXJ4

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ID QYXJ4 PRELIMINARY: PRT: 8 AA.
AC QYXJ4
DI 01-NOV-1999 (TrEMBLrel. 12, Created)
DI 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DI 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE runt/MTG8 protein (Fragment).
GN RNT/MTG8.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95002916; PubMed=7919324;
RA Tigue J.E., Calabi F.;
  "Alternative, out-of-frame runt/MTG8 transcripts are encoded by the
  derivative (6) chromosome in the t(8;21) of acute myeloid leukemia
  M2."
  Blood 84:2115-2121(1994).
DR EMBL: S74092; AAD14144.1; -.
FT NON-TER 1 1
SQ SEQUENCE 8 AA: 1067 MW: 20F414044B17244B AC64:

Query Match 40.0%; Score 2; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LE 2
DB 3 LE 4

RESULT 5
QYXJ3
ID QYXJ3 PRELIMINARY: PRT: 8 AA.
AC QYXJ3
DI 01-NOV-1999 (TrEMBLrel. 12, Created)
DI 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DI 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE runt/MTG8 protein (Fragment).
GN RNT/MTG8.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=BONE MARROW;
RX MEDLINE=95002916; PubMed=7919324;
RA Tigue J.E., Calabi F.;
  "Alternative, out-of-frame runt/MTG8 transcripts are encoded by the
  derivative (3) chromosome in the t(8;21) of acute myeloid leukemia
  M2."
  Blood 84:2115-2121(1994).
DR EMBL: S74094; AAD14973.2; -.
FT NON-TER 1 1
SQ SEQUENCE 8 AA: 229 MW: 20F764105B17344B AC64:

Query Match 40.0%; Score 2; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LE 2
DB 3 LE 4

RESULT 6
Q60773
ID Q60773 PRELIMINARY: PRT: 8 AA.
AC Q60773
DI 01-AUG-1998 (TrEMBLrel. 07, Created)
DI 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

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01-JUN-2001 (TReMBurel. 17, Last annotation update)
DE FF126310.1 (Parvalbumin) (Fragment)
GN FVALB.
OS Homo sapiens (Human).
OC Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
OC Mammalia, Eutheria, Primates, Catarrhini, Homiidae, Homo.
FN NCBI_TaxID=9606;
RX {}
OR SEQUENCE FROM N A
RA HO S.;
RBL Submitted (DEC-1999) To the EMBL/GenBank/CCDS databases.
DE EMBL_282184, CAB05699.3,
DF NON_TER 1 1
SQ SEQUENCE 8 AA: 454 MW: 99810.27 kDa: 99.54;

Query Match 45.3%; Score 2; 18 k; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0;

Q# 2 ES 3
  1 1
  7 ES 8

RESULT 7
Q94623
ID Q94623 PRELIMINARY: PRT: 8 AA
AC Q94623:
DT 01-FEB-1997 (TReMBurel. 02, Created)
DT 01-FEB-1997 (TReMBurel. 02, Last sequence update)
DE 01-NOV-1998 (TReMBurel. 08, Last annotation update)
DE MstSP-2 protein (Fragment).
OS USP
GN Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
OS Eukaryota, Metazoa, Arthropoda, Tracheata, Hexapoda, Insecta;
OC Pterygota, Neoptera, Endopterygota, Lepidoptera, Glossata, Ditrys
OC Spingidae, Spingidae, Spinginae, Manduca.
FN NCBI_TaxID=7130;
RX {}
OR SEQUENCE FROM N A.
RA RP
RBL TISSUE=EPIDERMIS;
RBL MEDLINE=97163493; PubMed=9013254;
DE Jinda M., Huang J.Y., Malone F., Asahina M., Piddford L.M.;
DE "Identification and mRNA developmental profiles of two ultraviolet
DE isoforms in the epidermis and wings of Manduca sexta.";
DE Insect Mol. Biol. 6:41-53 (1997).
DR EMBL; 05421. AAA4231.1.
FT NON_TER 8
  1 1
  SEQUENCE 8 AA: 892 MW: 116588.04 kDa: 98.04;

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FF SEQUENCE FROM N.A.
FX MEDLINE=9704932; PubMed=8894053;
FA Venter P.J., Broutet J.A., Yuzhasyan-Gurkan V., Brewer G.J.,
FR "Gene-specific universal mammalian sequence-tagged sites: application
RT to the canine genome."
RL Biochem. Genet. 34:321-341(1996).
RN [2]
RP SEQUENCE FROM N.A.
RPA Venter P.J., Cao Y., Alexander L., Yuzhasyan-Gurkan V.:
RT "Nucleotide repeat polymorphism in the canine retinoblastoma (RB1)
FT gene."
RPL Submitted (JUN-1999) to the EMBL/GenBank/Tran databases.
RDR EMBL: AF155737; AAD38807.1;
FE NON-TER 1
FT NON-TER 8
SQ SPQDNCF 6 AA 365 MW 1425ER:9676721E2 CRC64;

Query Match 45.0%; Score 2; FP 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ES 3
DB 11
7 ES 7

RESULT 9
Q9XNP8 PRELIMINARY; PRT; 8 AA.
ID Q9XNP8
AC Q9XNP8;
DT 01-NOV-1999 (TrEMBLrel. 12; Created)
DI 01-NOV-1999 (TrEMBLrel. 12; Last sequence update)
DE 01-NOV-1999 (TrEMBLrel. 12; Last annotation update)
DEF ATP synthase 6 (Fragment).
GN ATP6.
OS Bosophilus microplus (Cattle tick).
OC Mitochondrion.
OG Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Parasitiformes; Ixodida; Ixodidae; Boophilus.
NCBI_ProtID=5941;
RN [1]
RP SEQUENCE FROM N.A.
RPA STAIN-N;
FR MEDLINE=920721; PubMed=1046952;
FA Campbell N.J.H., Barker S.C.;
FR "The novel mitochondrial gene arrangement of the cattle tick,
RT Bosophilus microplus (Ixodidae) through repetition of a coding region."
RPL Mol. Biol. Evol. 16:732-740(1999).
RDR EMBL: AF110616; AAD28386.1;
FE NON-TER 1
FT NON-TER 8 AA 115 MW 6864444P:3780 2P:34;
SQ SPQDNCF 8 AA 115 MW 6864444P:3780 2P:34;

Query Match 40.0%; Score 2; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ES 3
DB 11
7 ES 8

RESULT 10
Q34909 PRELIMINARY; PRT; 8 AA.
ID Q34909
AC Q34909;
DT 01-NOV-1996 (TrEMBLrel. 01; Created)
DI 01-NOV-1996 (TrEMBLrel. 01; Last sequence update)
DE 01-DEC-1996 (TrEMBLrel. 15; Last annotation update)
DEF Cytochrome b (Fragment).
GN Cytochrome b.
OS Locusta migratoria (Migratory locust).
OC Mitochondrion.
OG Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;

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PT New peptides useful for inhibiting human immunodeficiency virus type 1
 PT (HIV-1) gp120 induced neuronal cell death
 XX
 XX Claim 1; Page 11; 10pp; English.
 XX
 CC AAY49695 and AAY49696 represent peptides which inhibit HIV-1 gp120
 CC induced neuronal cell death. Pharmaceutical compositions containing the
 CC peptides are useful for treating symptoms caused by neuronal cell loss.
 CC Such conditions especially associated with HIV infection include:
 CC encephalopathies, neuropathies, memory loss, dementia, depression,
 CC psychosis and opportunistic infections. The peptides act as antagonists
 CC of gp120-mediated neurotoxicity and subsequent neuronal degeneration.
 CC This enables therapeutic treatment of HIV infection and other
 CC inflammatory neurological diseases, including multiple sclerosis,
 CC tropical spastic paraparesis and Alzheimer's disease.
 XX
 XX Sequence 5 AA:
 XX
 Query Match 100.0%; Score 5; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LESYT 5
 IIII
 DB 1 LESYT 5
 RESULT 2
 AAY98253
 ID AAY98253 standard; Peptide: 4 AA.
 XX
 AC AAY98253;
 XX
 DT 24-JAN-2002 (first entry)
 XX
 DE Human peptide #1528 encoded by a SNP oligonucleotide.
 XX
 KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
 KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
 KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
 KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
 KW complement related protein; cytochrome; kinase; cytokine; interferon;
 KW interleukin; G-protein coupled receptor; thymesterase; inflammation;
 KW multifactorial disease; autoimmune disease; infection;
 KW nervous system disease.
 XX
 XX Homo sapiens.
 OS
 WO200147944-A2.
 XX
 PD 05-JUL-2001.
 XX
 PF 28-DEC-2000; 2000WO-0535498.
 XX
 FR 28-DEC-1999; 9908-0173419.
 PR 27-DEC-2000; 2000US-0173419.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 FI Shinkets RA, Leach M;
 XX
 DR WPI: 2001-465210/50.
 XX
 PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
 PT oncogenes and histones, useful for diagnosis and treating, e.g.
 PT cancer, autoimmune diseases and infections
 XX
 PS Disclosure; Page 4003; 4143pp; English.
 XX
 CC The present invention relates to oligonucleotides (see AAL26793; AAL34659)
 CC encoding polymorphic variants of proteins related to amylases, amyloid
 CC proteins, angiotensin, apoptosis related proteins, cadherin, cyclin,
 CC polymerase, oncogenes, histones, kinases, colony stimulating factors,

CC complement related proteins, cytochromes, kinesins, cytokines,
 CC interferons, interleukins, G-protein coupled receptors and thioesterases.
 CC The present sequence is a peptide encoded by one such oligonucleotide.
 CC The oligonucleotides and the peptides encoded by them may be used in the
 CC prevention, diagnosis and treatment of diseases associated with... that may
 CC inactivate expression of the proteins listed above. Disorders that may
 CC be prevented, diagnosed and/or treated include multifactorial diseases
 CC with a genetic component, such as autoimmune diseases (e.g. rheumatoid
 CC arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus
 CC and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,
 CC liver, breast, colon and kidney, leukaemia), diseases of the nervous
 CC system and an infection of pathogenic organisms.
 XX
 XX Sequence 9 AA:
 XX
 Query Match 80.0%; Score 4; DB 22; Length 9;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LESY 4
 IIII
 DB 2 LESY 5
 RESULT 3
 ABB55971
 ID ABB55971 standard; Peptide: 10 AA.
 XX
 AC ABB55971;
 XX
 DT 15-FEB-2002 (first entry)
 XX
 DE Vascular dementia-associated protein isoform (VPI) 171.
 XX
 KW Vascular Dementia; VD: VD-associated protein isoform; VPI: screening;
 KW diagnosis; prognosis; gene therapy;
 XX
 OS Homo sapiens.
 XX
 PN WO200169261-A2.
 XX
 PD 20-SEP-2001.
 XX
 PF 14 MAR 2001; 2001WO-GB01116.
 XX
 FR 15-MAR 2000; 2000GR-0004204.
 PR 24-NOV 2000; 2000AR-6028734.
 PR 28-NOV-2000; 2000US-0724391.
 XX
 PA (OXFORD) OXFORD GLYCOSCIENCES UK LTD.
 XX
 FI Horath HMAG, Parekh RB, Rohlf C;
 XX
 DR WPI: 2001-257937/42.
 XX
 PT Screening, diagnosis or prognosis of vascular dementia (VD) useful for
 PT determining stage of VD and monitoring the effect of VD therapy;
 PT comprises analysing body fluid by 2-dimensional electrophoresis for
 PT features correlated with VD
 XX
 PS Claim 6; Page 33; 151pp; English.
 XX
 CC The invention relates to screening, diagnosis or prognosis of Vascular
 CC Dementia (VD) in a subject comprising analysing body fluid from the
 CC subject by 2-dimensional (2-D) electrophoresis to generate a 2-D array of
 CC features containing at least one chosen feature whose relative abundance
 CC correlates with the presence, absence, stage or severity of VD or
 CC predicts the onset or course of VD, especially detecting in a sample of
 CC cerebrospinal fluid (CSF) from the subject one of 223 VD-associated
 CC protein isoforms (VPIs) (ABB55971; ABB56245) as fully defined in the
 CC specification. Detecting VD-associated features and VPI is useful for the
 CC screening, diagnosis or prognosis of VD, for determining the stage or
 CC severity of VD, for identifying a subject at risk of VD or for

CC monitoring the effect of therapy administered to a subject having VD.
 CC Nucleic acids encoding a VPI or inhibiting the function of a VPI are
 CC useful for the treatment of VD and for gene therapy.

XX SQ Sequence 10 AA:

Query Match 90.0%; Score 4; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.3e-02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LESY 4
 ||||
 Db 3 LESY 6

RESULT 4

ABR52194
 ID ABR52194 standard; Peptide: 10 AA.

XX AC ABR52194;

1 08-FEB-2002 (first entry)

XX DE Human API-149 tryptic digest peptide #2.

XX KW Human; neuroprotective; neurotropic; gene therapy; vaccine;

XX KW Alzheimer's disease; Alzheimer's Disease-Associated Feature; AF;

XX KW Alzheimer's Disease-Associated Protein Isoform; API; tryptic digest;

XX KW Expression Reference Protein Isoform; ERPI; proteolysis.

XX OS Homo sapiens.

XX PN W0200175454-A2.

XX XX 11-OCT-2001.

XX PF 03-APR-2001; 2001WO-0510408.

XX PP 03-APR-2000; 2000US-104504P

XX PR 26-NOV-2000; 2000US-253647P.

XX XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

XX PA (PF12) PFIZER INC.

XX XX Durham KL, Friedman DL, Herath HM, Kimmel LH, Parekh PR;

XX PI Potter DM, Rohlff C, Silber BM, Stiger IK, Sunderland PI;

XX PI Townsend RP, White F, Williams SA;

XX XX WPI: 2001-600484/74.

PI Screening for Alzheimer's disease in a mammalian by making
 PT two-dimensional array of a feature whose relative abundance correlates
 PI with disease, and comparing with abundance of the feature in samples of
 PT healthy persons -

XX Example; Page 49; 162pp; English.

XX The invention relates to methods for the screening, diagnosis and
 CC prognosis of Alzheimer's disease. The methods involve the detection
 CC of Alzheimer's Disease-Associated Features (AFs) and Alzheimer's
 CC Disease-Associated Protein Isoforms (APIs) in cerebrospinal fluid,
 CC serum or plasma. The abundance of the AFs and APIs is then
 CC normalised to an Expression Reference Protein Isoform (ERPI) in
 CC order to determine whether a patient is suffering from, or has
 CC a predisposition to, Alzheimer's Disease. The relative abundance of
 CC the AFs and APIs correlates with the severity of Alzheimer's Disease.
 CC The present sequence is a peptide produced from an API by proteolysis.

XX SQ Sequence 10 AA:

Query Match 80.0%; Score 4; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.3e-02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LESY 4
 ||||
 Db 3 LESY 6

RESULT 5

AAU28456

ID AAU28456 standard; Peptide: 10 AA.

XX AC AAU28456;

XX DT 03-JAN-2002 (first entry)

XX DE DPI tryptic digest peptide #53.

XX KW Human; depression associated protein isoform; tryptic digest peptide-

XX KW buf; cerebrospinal fluid; CSF; NAD; bipolar affective disorder;

XX KW neuropsychiatric disorder; bipolar mood disorder; neuroleptic;

XX KW manic depressive illness; schizoaffective disorder.

XX OS Homo sapiens.

XX PR W0200162787-A1.

XX PD 30-AUG-2001.

XX PF 23-FEB-2001; 2001WO-0900786.

XX PR 24-FEB-2000; 2000GB-0004112.

XX PR 04-DEC-2000; 2000GR-0030050.

XX PR 12-DEC-2000; 2000US-0254830.

XX PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

XX PI Herath HM, Parekh PR, Rohlff C, Terrett JA, Tyson KL;

XX DE WPI: 2001-570626/64.

XX Novel novel-10 acid encoding a protein associated with bipolar affective
 PT disorder, which is used for diagnosis, prophylaxis and therapy of
 PI neuropsychiatric disorders, such as bipolar affective disorder -

XX Disclosure; Page 31; 153pp; English.

XX The present invention relates to the identification of depression
 CC associated protein isoforms (DPIs), particularly the tryptic digest
 CC peptides of these proteins. Some of the DPIs (AAU28404-AAU28425)
 CC described are decreased in the cerebrospinal fluid (CSF) of BAP
 CC (bipolar affective disorder) subjects, whilst other DPIs
 CC (AAU28426-AAU28487) are increased in BAP subjects. Also described
 CC are peptide sequences identified from DPI-45 and DPI-213 and the
 CC nucleic acid sequences they are encoded by. The sequences of the
 CC invention are useful for clinical screening, diagnosis, prognosis,
 CC therapy and prophylaxis of neuropsychiatric disorders e.g. BAP (also
 CC known as bipolar mood disorder, BP), manic-depressive illnesses,
 CC attention deficit disorders, schizoaffective disorders, and unipolar
 CC affective disorders. The present sequence represents one of the DPI
 CC tryptic digest peptides of the present invention.

XX SQ Sequence 10 AA:

Query Match 80.0%; Score 4; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.3e-02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LESY 4
 ||||
 Db 3 LESY 6

RESULT 6

AAU25102

1D AAU26102 standard; Peptide: 10 AA
 XX
 AC AAU26102;
 XX
 DI 18-DEC-2001 (first entry)
 XX
 DE Depression-Associated Protein isoform DPI-1;
 XX
 DE Human; Bipolar Affective Disorder; BAD; Depression-Associated Protein;
 XX
 DE Depression-Associated Protein isoform; BAD; Cerebrospinal fluid;
 XX
 DE CSF; antidepressant; antimanic; neuroleptic; tranquiliser; neuroleptic;
 XX
 DE attention deficient disorder; schizoaffective disorder;
 XX
 DE bipolar affective disorder;
 XX
 OS Homo sapiens;
 XX
 PN W0200163294-A2;
 XX
 PD 30-AUG-2001;
 XX
 PD 23-FEB-2002; 2201W0-GB00791;
 XX
 PR 24-FEB-2000; 2300GH-0004412;
 PR 08-DEC-2000; 2300GB-0030650;
 PF 12-SEP-2000; 2300JS-0254830;
 XX
 XX (OXFORD) EXP-PRO-CLIN SCIENCES UK LTD
 PA Herath HMAC, Parekh FB, Rohlf C;
 PI
 XX WPI: 2001-582081/65;
 DR
 XX Preparation for diagnosing or treating bipolar affected disorder (BAD)
 PI or unipolar depression, or for screening for modulators, comprises a
 PT BAD-associated protein isoform;
 XX
 PS Claim 8; Page 31; 163pp; English;
 XX
 CC The invention relates to a preparation comprising an isolated Bipolar
 CC Affected Disorder (BAD)-Associated Protein Isoform (DPI). The DPI's are
 CC used to screen, diagnose or prognosis of BAD or unipolar depression,
 CC determine the stage or severity of BAD or unipolar depression, identify a
 CC subject at risk of developing BAD or unipolar depression, or monitor the
 CC effect of therapy in a subject. They are also used to screen for or
 CC identify agents that interact with a DPI. These agents, antibodies
 CC against the DPIs, and nucleic acids encoding the DPIs are used to treat
 CC or prevent BAD or unipolar depression. Diseases that can be treated are
 CC attention deficient disorder, a schizoaffective disorder, a bipolar or a
 CC unipolar affective disorder. The DPIs are used in proteomics. The
 CC proteomic approach of using DPIs for screening, diagnosis or prognosis of
 CC BAD or unipolar depression overcomes the problems of using gene
 CC expression analysis, such as not being able to obtain central nervous
 CC system (CNS) tissue from a living patient under normal circumstances.
 CC The present sequence is a DIP decreased in the CSF (cerebrospinal
 CC fluid) of subjects having BAD.
 XX
 SQ Sequence 10 AA;
 Query Match: 80.0%; Score 4; DB 10; Length 10;
 Best Local Similarity 100.0%; Pred No. 133412;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LESY 4
 DL 3 LESY 6
 RESULT 7
 AAY20715
 1D AAY20715 standard; Protein: 4 AA.
 XX
 AC AAY20715;
 XX

PI 22-MAY-1998 (first entry)
 XX
 DE Human neurofilament-M wild type protein fragment 57;
 XX
 KW Human; beta-amyloid precursor protein; beta-APP; diagnosis; cancer;
 KW frameshift mutation; age-related disease; neurodegenerative disorder;
 KW Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal;
 KW Huntington's disease; multiple sclerosis; alcoholic liver disease;
 KW diabetes mellitus type II; microtubule associated protein; Tau; Big Tau;
 KW neurofilament; neurofilament E; MAP2; neurofilament; neurofilament-M;
 KW neurofilament-F; presenilin 1; presenilin 2; cellular tumor antigen;
 KW glial fibrillary acidic protein; GFAP; p53; semaphorin III; HSP-70;
 KW 1-12 kDa; neurofilament; neurofilament; neurofilament; neurofilament;
 KW high mobility group protein-C; neuroendocrine specific protein A;
 XX
 OS Homo sapiens;
 XX
 PN W09845322-A2;
 XX
 PD 15-OCT-1998;
 XX
 PD 02-APR-1998; 96W0-IB00705;
 XX
 PR 10-APR-1997; 97US-0043163;
 XX
 XX (UYUT-) RIJCKSUNIV UTRECHT;
 PA (UYUT-) RIJCKSUNIV UTRECHT;
 PA (UYUT-) RIJCKSUNIV UTRECHT;
 PA (UYUT-) RIJCKSUNIV UTRECHT;
 XX
 PI Burbach JPH, Grosveld FG, Van Leeuwen FW;
 XX
 XX WPI: 1998-609901/51;
 DR N-PSDB: AAX75759;
 DR
 XX Diagnosing disease by detecting frameshift mutations in PNA or
 PT corresponding protein mutations - used to diagnose cancer and
 PT neurological diseases, particularly Alzheimer's disease, and also
 PT for treatment and prevention with specific ribozymes or wild-type
 PT RNA
 XX
 PS Disclosure: Figure 8; 258pp; English;
 XX
 CC This invention describes a novel method for the diagnosis of a disease
 CC caused by, or associated with, an RNA molecule that has a frameshift
 CC mutation. The method is used to diagnose age-related diseases, especially
 CC cancer and a wide range of neurodegenerative disorders (e.g. Alzheimer's
 CC disease, Down's syndrome, myotonic dystrophy, Huntington's disease,
 CC multiple sclerosis, alcoholic liver disease, diabetes mellitus type II
 CC and many others listed), or susceptibility to these disorders. The method
 CC allows a definitive diagnosis of Alzheimer's disease in living patients,
 CC at an early stage. It is based on the observation that disease may be
 CC caused by mutations in RNA rather than DNA. The invention describes the
 CC used of neuronal system RNA molecules, specifically proteins including
 CC beta amyloid precursor protein (beta-APP), the microtubule associated
 CC proteins Tau and Big Tau, ubiquitin B, apolipoprotein E, microtubule
 CC associated protein 2 (MAP2), neurofilament-L, neurofilament-M,
 CC neurofilament-F, presenilin 1, presenilin 2, glial fibrillary acidic
 CC protein (GFAP), the cellular tumour antigen p53, B-cell leukemia/lymphoma
 CC 2 (BCL2), 12-O-tetradecanoyl phorbol-13-acetate 12-O-tetradecanoyl
 CC protein-C (HMGP-C) and neuroendocrine specific protein A.
 XX
 SQ Sequence 4 AA;
 Query Match: 60.0%; Score 3; DB 19; Length 4;
 Best Local Similarity 100.0%; Pred No. 780-05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 ESY 4
 DL 1 ESY 3
 RESULT 8

AAY20656
 ID AAY20656 standard; Protein: 4 AA.
 AC AAY20656;
 XX
 DT 22-JUL-1999 (first entry)
 DE Human neurofilament-L wild type protein fragment 46.
 DE
 XX Human; beta-amyloid precursor protein; beta-A4; diagnosis: cancer;
 KW frameshift mutation; age-related disease; neurodegenerative disorder;
 KW Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal;
 KW Huntington's disease; multiple sclerosis; alcoholic liver disease;
 KW diabetes mellitus type II; microtubule associated protein; Tau; Big Tau;
 KW ubiquitin B; apolipoprotein E; MAP2; neurofilament-L; neurofilament-M;
 KW neurofilament-F; presenilin 1; presenilin 11; cellular tumour antigen;
 KW glial fibrillary acidic protein; GFAP; p53; smaphorin III; HSP-1;
 KW bel-2; B-cell leukemia/lymphoma 2 proto-oncogene; HMGP-C; NSP-A;
 KW high mobility group protein-C; neuroendocrine specific protein A.
 XX
 XX Homo sapiens.
 XX
 PR W09845322-A2.
 XX
 PU 15-OCT-1998.
 XX
 DE 02-APR-1998; 98WO-1B00705
 XX
 PR 10-APR-1997; 97OS-0043163.
 XX
 XX (UYUT-) PIJRSUNIV UTRECHT.
 PA (ROYA-) ROYAL NETHERLANDS ACAD APTS & SCI.
 PA (UYRO-) UNIV ROTTERDAM ERASMUS.
 XX
 FI Rurbach JPH, Grosveld FG, Van Leeuwen FW;
 XX WPI: 1998-60990/51.
 DR N-PSDB; AAX75758.
 DR
 XX Diagnosing disease by detecting frameshift mutations in RNA or
 PT corresponding protein mutations - used to diagnose cancer and
 PT neurological diseases, particularly Alzheimer's disease, and also
 PT for treatment and prevention with specific polymers of wild-type
 PT RNA
 PS Disclosure: Figure 7: 258pp; English.
 XX
 CC This invention describes a novel method for the diagnosis of a disease-
 CC caused by, or associated with, an RNA molecule that has a frameshift
 CC mutation. The method is used to diagnose age related diseases, especially
 CC cancer and a wide range of neurodegenerative disorders (e.g. Alzheimer's
 CC disease, Down's syndrome, myotonic dystrophy, Huntington's disease,
 CC multiple sclerosis, alcoholic liver disease, diabetes mellitus type II
 CC and many others listed) or susceptibility to these disorders. The method
 CC allows a definitive diagnosis of Alzheimer's disease in living patients,
 CC at an early stage. It is based on the observation that disease may be
 CC caused by mutations in RNA rather than DNA. The invention describes the
 CC use of neuronal system RNA molecules, specifically proteins including
 CC beta-amyloid precursor protein (beta-APP), the microtubule associated
 CC proteins Tau and Big Tau, ubiquitin B, apolipoprotein E, microtubule
 CC associated protein 2 (MAP2), neurofilament-L, neurofilament-M,
 CC neurofilament-F, presenilin 1, presenilin 11, glial fibrillary acidic
 CC protein (GFAP), the cellular tumour antigen p53, B-cell leukemia/lymphoma
 CC 2 (bel-2) proto-oncogene, smaphorin III, Hsp-1, high mobility group
 CC protein-C (HMGP-C) and neuroendocrine specific protein A.
 XX
 XX Sequence 4 AA:
 XX
 Query Match 60.0%; Score 3; DB 19; Length 4;
 Best Local Similarity 100.0%; Pred. No. 7,8e-05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 SYT 5

III
 Db 1 SYT 3
 RESULT 9
 AAE08624
 ID AAE08624 standard; peptide: 4 AA.
 XX
 AC AAE08624;
 XX
 DT 01-NOV-2001 (first entry)
 XX
 DE Peptide for analysis; T-cell proliferative activity of human p35/p40.
 DE
 XX Cytokines; T-cell; interferon-gamma; IFN gamma; bacterial infection;
 KW AIDS; diabetic retinopathy; cancer; vaccine; cell-mediated immunity;
 KW p35; p40.
 KW
 XX Synthetic.
 GS
 XX W0200140257-A2.
 PN
 XX 07-JUN-2001.
 PD
 XX 30-NOV-2000; 2000WO-US32664.
 PF
 XX 02-DEC-1999; 99US-0169035.
 PP
 PR 28-NOV-2000; 2000US-0169035.
 XX
 XX (MAXY-) MAXYGEN INC.
 PA
 XX Leong SK, Punnonen J;
 PI
 XX WPI: 2001-502381/55.
 DR
 XX Nucleic acids encoding modified cytokine polypeptides (i.e. modified
 PT p40 and p35 polypeptides), useful for treating various diseases e.g.
 PT diabetic retinopathy and cancer.
 PT
 XX Disclosure: Page 41: 223pp; English.
 ES
 XX The invention relates to nucleic acids encoding modified cytokine
 CC polypeptides (i.e. modified p40 and p35 polypeptides). The modified
 CC cytokine polypeptides have T-cell proliferative and interferon (IFN)-
 CC gamma induction activities. The polypeptides and polynucleotides of the
 CC invention are useful for treating various diseases e.g. bacterial
 CC infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
 CC polynucleotide may also be useful as a vaccine adjuvant, to enhance a
 CC vaccinated host's cell-mediated immunity for protective response to a
 CC pathogen. The present sequence is a peptide used in the study of
 CC T-cell proliferative activity of human cytokine p35/p40.
 XX
 XX Sequence 4 AA:
 XX
 Query Match 60.0%; Score 3; PB 22; Length 4;
 Best Local Similarity 100.0%; Pred. No. 7,8e-05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LES 3
 III
 Db 1 LES 3
 RESULT 10
 AAF71550
 ID AAF71550 standard; Protein: 5 AA.
 XX
 AC AAF71550;
 XX
 DT 07-MAY-1991 (first entry)
 XX
 DE AIDS virus receptor site blocking peptide (III).
 DE
 XX

FW AIDS virus, recombinant site- HIV, vaccine, antibodies.

XX Synthetic.

XX EP249390-A.

XX 16-DEC-1987.

XX 03-JUN-1987; 87EP-0304913.

XX 11-MAY-1987; 87US-0048148.

XX 03-JUN-1986; 86US-0869919.

XX 26-JUN-1986; 86US-0878586.

XX 12-DEC-1986; 86US-0940919.

XX 03-JUN-1987; 87EP-0304913.

XX (PERT/) PERT C B.

XX (USDC) US SEC OF COMMERCE.

XX Pert CB, Ruff MR, Farrar WL;

XX WPI: 1987-350068/50.

XX New peptide(s) related to AIDS virus - which inhibit AIDS virus

XX binding to receptor sites and prevent cell infectivity with AIDS

XX virus

XX Claim 5; Page 9; 12pp; English.

XX This peptide is a specifically claimed example of a highly

XX generic formula.

XX The peptide blocks effectively receptor sites of

XX cells and prevents cell infectivity with AIDS virus in monkey, rat

XX and human brain membranes and cells of the immune system.

XX Vaccine preps. contg. the peptide provide protection against

XX infection by AIDS virus. The peptide can also be used in kits for

XX the detection of the AIDS virus and antibodies to the AIDS virus;

XX and as immunogens to elicit monoclonal antibodies.

XX The peptide may be produced by conventional methods of peptide

XX synthesis using solid phase or liquid phase methods.

XX See also AAP71548-56, and EP-249394.

XX Sequence 5 AA;

SQ

Query Match 60.0%; Score 3; DB 8; Length 5;

Best Local Similarity 100.0%; Pred. No. 7.8e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 3 SYT 5

III

3 SYT 5

RESULT 11

AAP71551

ID AAP71551 standard; Protein: 5 AA.

XX AAP71551;

XX 07-MAY-1991 (first entry)

XX AIDS virus receptor site blocking peptide (IV).

XX AIDS; virus; receptor site; HIV; vaccine; antibodies.

XX Synthetic.

XX EP249390-A.

XX 16-DEC-1987.

XX 03-JUN-1987; 87EP-0304913

XX WPI: 1987-350068/50.

XX Monoclonal antibodies and peptide(s) useful for treatment and

XX

FR 11-MAY-1987; 87US-0048148.

FR 03-JUN-1986; 86US-0869919.

FR 26-JUN-1986; 86US-0878586.

FR 12-DEC-1986; 86US-0940919.

FR 03-JUN-1987; 87EP-0304913.

XX (PERT/) PERT C B.

XX (USDC) US SEC OF COMMERCE.

XX Pert CB, Ruff MR, Farrar WL;

XX WPI: 1987-350068/50.

XX New peptide(s) related to AIDS virus - which inhibit AIDS virus

XX binding to receptor sites and prevent cell infectivity with AIDS

XX virus

XX Claim 5; Page 9; 12pp; English.

XX This peptide is a specifically claimed example of a highly

XX generic formula.

XX The peptide blocks effectively receptor sites of

XX cells and prevents cell infectivity with AIDS virus in monkey, rat

XX and human brain membranes and cells of the immune system.

XX Vaccine preps. contg. the peptide provide protection against

XX infection by AIDS virus. The peptide can also be used in kits for

XX the detection of the AIDS virus and antibodies to the AIDS virus;

XX and as immunogens to elicit monoclonal antibodies.

XX The peptide may be produced by conventional methods of peptide

XX synthesis using solid phase or liquid phase methods.

XX See also AAP71548-56, and EP-249394.

XX Sequence 5 AA;

SQ

Query Match 60.0%; Score 3; DB 8; Length 5;

Best Local Similarity 100.0%; Pred. No. 7.8e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYT 5

III

3 SYT 5

RESULT 12

AAP83009

ID AAP83009 standard; Protein: 5 AA.

XX AAP83009;

XX 10-DEC-1990 (first entry)

XX Blocking peptide used in composition for treatment and diagnosis

XX of HIV infections.

XX HIV; gp120; monoclonal antibodies; neutralising region.

XX Homo sapiens.

XX GB2196634-A.

XX 05-MAY-1988.

XX 19-AUG-1987; 87GB-0719587.

XX 29-JUN-1987; 87US-0067996.

XX 01-MAY-1987; 87US-0045026.

XX 20-AUG-1986; 86US-0898273.

XX (GENE-) GENETIC SYSTEMS COR.

XX WPI: 1988-103268/15.

XX Monoclonal antibodies and peptide(s) useful for treatment and

XX

PT diagnosis of human immuno-deficiency virus infections

XX Claim 42; Page 24; 25pp; English.

XX This is a blocking peptide which inhibits virus proliferation.

CC It is useful, in conjunction with a monoclonal antibody to a

CC neutralising region of HIV, for treatment or prophylaxis of HIV

CC infections. N- and C-terminals can have up to 20 amino acids attached.

CC See also AAP8003-08 and AAP84010-12.

CC This is equivalent to MLR701259 (accession no. is from this).

XX Sequence 5 AA:

Query Match 60.0%; Score 3; DP 9; Length 5;

Best Local Similarity 100.0%; Pred. No. 7.8e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYT 5

DB 3 SYT 5

RESULT 13

AAP91855

ID AAP91855 standard; protein: 5 AA.

XX AAP91855;

XX 17-DEC-2001 (updated)

DT 22-MAY-1990 (first entry)

XX Pentapeptide which inhibits HIV binding to cell surface receptors.

DE HIV; psoriasis; neuropsychiatric disorders.

XX USN7352313-N.

XX 10-OCT-1989.

XX 16-MAY-1989; E9NS-0212648.

XX 16-MAY-1989; E9NS-0352313.

XX (USSH) US LEPT HEALTH AND HUMAN.

XX Bridge P, Goodwin FR,

XX WPI: 1989-378087-51.

PT Use of short peptide(s) to inhibit binding of HIV to human cells for

XX treating psoriasis and neuropsychiatric disorder including memory

XX deficiency and mood disorder.

XX Disclosure; Page 8; 18pp; English.

CC This peptide is used in a composition for treatment of brain conditions

CC eg neuropsychiatric disorders and psoriasis through inhibition of HIV

CC cell surface receptor (CD4) binding. CD4 site is common to the CNS and

CC immune system. AIDS- and non AIDS-related psoriasis both respond

CC favourably to treatment with the peptide-containing composition. There

CC are a range of forms which the composition and administration can take.

CC The serine residue can be replaced by an asparagine residue. Analogues

CC of these peptides with D-threonine as the amino-terminal residue and/or

CC an amide derivative at the carboxy-terminal can also be used.

CC (Note: Revised entry submitted to correct the patent number format of

CC US Government-owned NTIS applications to prevent clashes with ongoing US

CC granted patent numbers. For further information please visit the Derwent

XX web site at www.derwent.com/dwpl/updates/ntis-us-hcm1)

XX Sequence 5 AA:

Query Match 60.0%; Score 3; DP 10; Length 5;

Best Local Similarity 100.0%; Pred. No. 7.8e+05.

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYT 5

DB 3 SYT 5

RESULT 14

AAP26903

ID AAP26903 standard; peptide: 5 AA.

XX AAP26903;

XX 20-MAY-1998 (first entry)

XX Herpes simplex virus treatment peptide.

XX HSV; HSV-1; HSV-2; Varicella Zoster virus; human cytomegalovirus;

XX Epstein-Barr virus.

XX Synthetic.

XX WO9214751-A.

XX 03-SEP-1992.

XX 24-FEB-1992; 92WO-DE00053.

XX 25-FEB-1991; 91DK-0000319.

XX (CARL-) CARLBIO TECH LTD-AS.

XX MacLadden DK, Pedersen G

XX WPI: 1992-315120/28.

XX New linear or cyclic peptide(s) including cysteine residue

XX PT occupy lymphocyte CD4 receptors, for treating and preventing

XX PT virus infections with Herpes simplex Varicella Zoster

XX PT cytomegalovirus and Epstein-Barr virus

XX Claim 5; Page 15; 21pp; English.

XX The peptide is useful in the treatment and prevention of diseases or

XX conditions caused by Herpes viruses, esp. Herpes Simplex Virus-1

XX (HSV-1), HSV-2, Varicella Zoster Virus (VZV), human cytomegalovirus

XX (HCMV) or Epstein-Barr Virus (EBV). It can also be used to treat

XX diseases and conditions caused by the family of herpes viruses in

XX animals, e.g. Rubella's disease in pigs, bovine rhinotracheitis

XX (BVD), lymphogranuloma venereum, lymphogranuloma venereum and

XX disease in chickens. It can also be used in diagnostics. The peptide

XX has never been reported to penetrate any type of cells, but only to

XX occupy the CD4 receptors found on lymphocytes and it apparently

XX penetrates the skin with relative ease. A major advantage of the

XX peptide is its almost complete lack of toxicity, which means that the

XX use of high doses for an extended period of time is possible without

XX any drawbacks. It is an example of a highly generic peptide

XX (AAP26903). See also AAP26903-026906.

XX Sequence 5 AA:

Query Match 60.0%; Score 3; DP 13; Length 5;

Best Local Similarity 100.0%; Pred. No. 7.8e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYT 5

DB 3 SYT 5

RESULT 15

AAR28941

ID AAR28941 standard; peptide: 5 AA.

XX AAR28941;
XX 23-MAR-1993 (first entry)
XX Example of a generic peptide for treating chronic fatigue syndrome.
DE CFS; fatigue; tension; anger; confusion; peptide T; HIV; synthetic;
KW human immunodeficiency virus; gp 120.
XX Synthetic.
XX Key Location/Qualifiers
FH Misc-difference 1 /note- "Thr or D-Thr"
FT Modified-site 5 /note- "may be amidated"
FI
FI
XX WO9219257-A.
XX 12-NOV-1992.
XX 08-MAY-1992; 92WO-US03582.
XX 04-MAY-1991; 91US-0696556.
XX (USSH) US DEPT HEALTH & HUMAN SERVICE.
XX Bridge TP. Goodwin FK;
XX WPI: 1992-398545/48.
XX Peptide compns. for treating chronic fatigue syndrome.
PT ameliorate symptoms and improve vigour and cognitive and
PT neuro-motor performance
XX Disclosure; Page 4; Zipp; English.
XX The synthetic peptide is an example of a generic peptide whose
sequence is based on the sequence of peptide T, a sub region of
CC HIV gp120 responsible for binding to brain membrane and human T
cells. The peptide may be used for treatment of chronic fatigue
CC syndrome not associated with HIV infection. The peptide will reduce
CC fatigue, tension, anger and confusion and improves cognitive and
CC neuromotor performance.
CC See also AAR28918-42.
XX Sequence 5 AA;

Query Match 60.0%; Score 3; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. NO. 7.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 SYT 5
DB 3 SYT 5

Search completed: April 29, 2003, 08:51:53
Job time : 44.0833 secs

TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 247:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-071-838-247

Query Match 60.0% Score 3: DB 10: Length 4:
Best Local Similarity 100.0% Pred. No. 2.7e-05: Indels 0:
Matches 3: Conservative 3: Mismatches 0: Gaps 0:

QY 3 SYT 5
|||
DB 1 SYT 3

US-09-286-240-20
Sequence 20, Application US/99286240
Patent No. US2002010420A1
GENERAL INFORMATION:
APPLICANT: Pett, James W
TITLE OF INVENTION: Chimeric and Humanized Anti-IL-13 to Angiogenic
FILE REFERENCE: 10498740/3
CURRENT APPLICATION NUMBER: US 09/286,240
CURRENT FILING DATE: 1999-04-05
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 20
LENGTH: 5
TYPE: PRT
ORGANISM: Mus musculus
FEATURE:

US-09-286-240-20

Query Match 60.0% Score 3: DB 10: Length 5:
Best Local Similarity 100.0% Pred. No. 2.7e-05: Indels 0:
Matches 3: Conservative 3: Mismatches 0: Gaps 0:

QY 3 SYT 5
|||
DB 1 SYT 3

US-09-828-708-17
Sequence 17, Application US/99286240
Patent No. US20020146753A1
GENERAL INFORMATION:
APPLICANT: Dittel H.
APPLICANT: Bottom D.
APPLICANT: Schaller M.
TITLE OF INVENTION: Autoantibodies to glucose 6-phosphate isomerase and their partici
FILE REFERENCE: 1361.005051
CURRENT APPLICATION NUMBER: US/99-828-708
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 123
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 17
LENGTH: 5
TYPE: PRT
ORGANISM: Homo sapiens
US-09-828-708-17

Query Match 60.0% Score 3: DB 10: Length 5:
Best Local Similarity 100.0% Pred. No. 2.7e-05: Indels 0:
Matches 3: Conservative 0: Mismatches 0: Gaps 0:

QY 3 SYT 5
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DB 1 SYT 3

RESULT 8

US-09-953-031A-8
Sequence 8, Application US/99953031A
Patent No. US2002017717A1
GENERAL INFORMATION:
APPLICANT: Bernards, Rene
APPLICANT: Zwijssen, Renate
TITLE OF INVENTION: Interaction Between Cyclin D1 and Steroid Receptor
FILE REFERENCE: 4238/80713
CURRENT APPLICATION NUMBER: US/99-953-031A
CURRENT FILING DATE: 2001-12-05
PRIOR APPLICATION NUMBER: US 09/302,305
PRIOR FILING DATE: 1999-04-10
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 8
LENGTH: 6
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (1)-(6)
CITE INFORMATION: B 9:330-3:116 IL LXXIX motif
US-09-953-031A-8

Query Match 60.0% Score 3: DB 9: Length 6:
Best Local Similarity 100.0% Pred. No. 2.7e-05: Indels 0:
Matches 3: Conservative 0: Mismatches 0: Gaps 0:

QY 1 LES 3
|||
DB 2 LES 4

RESULT 9

US-09-945-225-47
Sequence 47, Application US/9995225
Publication No. US20020193584A1
GENERAL INFORMATION:
APPLICANT: Chen, Ruoping
APPLICANT: Chu, Zhi Liang
APPLICANT: Dang, Huong T.
APPLICANT: Lowitz, Kevin P.
APPLICANT: Pride, Cameron
TITLE OF INVENTION: Enzymes And Re US20020193584A1 Publication Title of Huma
FILE REFERENCE: AREN-0308
CURRENT APPLICATION NUMBER: US/99-945-225
CURRENT FILING DATE: 2001-11-26
PRIOR APPLICATION NUMBER: 09/170,496
PRIOR FILING DATE: 1998-10-13
PRIOR APPLICATION NUMBER: 123,000,23338
PRIOR FILING DATE: 1998-10-13
PRIOR APPLICATION NUMBER: 60/282,358
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/255,366
PRIOR FILING DATE: 2000-12-12
PRIOR APPLICATION NUMBER: 60/270,286
PRIOR FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 60/282,358
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: 60/282,358
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: 60/282,356
PRIOR FILING DATE: 2001-04-06

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; PRIOR APPLICATION NUMBER: 60/200,317
; PRIOR FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 60/409,209
; PRIOR FILING DATE: 2001-07-31
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: Patent version 3.1
; SEQ ID NO 47
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. US20020193584A1el Sequence
US-09-995-225-47

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Query Match      60.0%; Score 3; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.7e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LJ 1 LES 3
    III
    2 LES 4

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RESULT 10
US-10-097-175-99
; Sequence 99, Application US/10097175
; Publication No. US20030045680A1
; GENERAL INFORMATION:
; APPLICANT: JOVAL, JOHN L.
; APPLICANT: MUELLER, JOHN
; APPLICANT: OLA, VIBHA B.
; TITLE OF INVENTION: FINDELS, MARK A
; FILE REFERENCE: PPI-110
; CURRENT APPLICATION NUMBER: US/10/097,175
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/275,240
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: 60/352,369
; PRIOR FILING DATE: 2002-01-28
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 99
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Androgen Receptor Binding Polypeptides
US-10-097-175-99

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Query Match      60.0%; Score 3; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.7e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY 2 ESY 4
    III
    2 ESY 4

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RESULT 11
US-09-984-292-40
; Sequence 40, Application US/09/984292
; Patent No. US20020128433A1
; GENERAL INFORMATION:
; APPLICANT: XU, HONG
; APPLICANT: YAO, YONG
; TITLE OF INVENTION: G-ALPHA-0 PROTEIN VARIANT AND THEIR USE IN THE
; TITLE OF INVENTION: ANALYSIS AND DISCOVERY OF AGONISTS AND ANTAGONISTS OF
; TITLE OF INVENTION: CHEMOSENSORY RECEPTORS
; FILE REFERENCE: 078003-0280649
; CURRENT APPLICATION NUMBER: US/09/984,292
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 60/243,770

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; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 40
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Illustrative
; OTHER INFORMATION: N-terminal peptide sequence
US-09-984-292-40

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```

Query Match      60.0%; Score 3; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.7e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 LES 3
    III
    3 LES 5

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RESULT 12
US-09-989-497-40
; Sequence 40, Application US/09989497
; Patent No. US20020143151A1
; GENERAL INFORMATION:
; APPLICANT: YAO, YONG
; APPLICANT: XU, HONG
; TITLE OF INVENTION: G-ALPHA-0 PROTEIN VARIANTS AND THEIR USE IN THE
; TITLE OF INVENTION: ANALYSIS AND DISCOVERY OF AGONISTS AND ANTAGONISTS OF
; TITLE OF INVENTION: CHEMOSENSORY RECEPTORS
; FILE REFERENCE: 078003-0280735
; CURRENT APPLICATION NUMBER: US/09/989,497
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/484,292
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 60/243,770
; PRIOR FILING DATE: 2001-10-29
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 40
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Illustrative
; OTHER INFORMATION: N-terminal peptide sequence
US-09-989-497-40

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Query Match      60.0%; Score 3; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.7e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 LES 3
    III
    3 LES 5

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RESULT 13
US-09-867-852-138
; Sequence 138, Application US/09867852
; Patent No. US/98/034752A1
; GENERAL INFORMATION:
; APPLICANT: Ausubel, Frederick M.
; APPLICANT: Staskawicz, Brian J.
; APPLICANT: Brent, Andrew F.
; APPLICANT: Fahlbeck, Douglas
; APPLICANT: Katagiri, Fumaki
; APPLICANT: Kunkel, Bailata N.
; APPLICANT: Mindrinos, Michael N.
; APPLICANT: Y. Gao-Liang
; TITLE OF INVENTION: PPS2 GENE FAMILY, PRIMERS, PROBES, AND
; TITLE OF INVENTION: DETECTION METHODS

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: FILE REFERENCE: 00786/254002
: CURRENT APPLICATION NUMBER: US/09/867,852
: CURRENT FILING DATE: 2001-05-29
: PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-28
: PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/301,085
: PRIOR FILING DATE: EARLIER FILING DATE: 1994-09-12
: PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/227,365
: PRIOR FILING DATE: EARLIER FILING DATE: 1994-04-13
: NUMBER OF SEQ ID NOS: 209
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 138
: LENGTH: 6
: TYPE: PRT
: ORGANISM: Arabidopsis thaliana
US-09-867-852-138

Query Match      60.0%; Score 3; DB 13; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.7e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db      1 LES 3
      III
      4 LES 5

RESULT 14
US-10-000-273-13
: Sequence 13: Application US/10000273
: Patent No. US20020160386A1
: GENERAL INFORMATION:
: TITLE OF INVENTION: NOVEL GENES ENCODING A GANGLIOSIDE BINDING MOLECULES
: NUMBER OF SEQUENCES: 17
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Fish & Richardson P.C.
: STREET: 225 Franklin Street
: CITY: Boston
: STATE: MA
: COUNTRY: USA
: ZIP: 02110-2804
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: Windows 95
: SOFTWARE: FastSeq for Windows Version 2.0b
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/10/000,273
: FILING DATE: 02-Nov-2002
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/09/964,127
: FILING DATE: 06-NOV-1997
: ATTORNEY/AGENT INFORMATION:
: NAME: Trex, Ph.D., L. Lee
: REGISTRATION NUMBER: P-43,567
: REFERENCE/KEYWORD NUMBER: 0734,048000
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 617/542-5070
: TELEFAX: 617/542-8906
: TELEX: 200154
: INFORMATION FOR SEQ ID NO: 13:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 7 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-10-000-273-13

Query Match      60.0%; Score 3; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.7e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db      1 LES 3
      III
      5 LES 7

RESULT 15
US-10-091-236-15
: Sequence 15: Application US/10001236
: Patent No. US20020168360A1
: GENERAL INFORMATION:
: APPLICANT: DINGIVAN, CHRISTINE A.
: TITLE OF INVENTION: METHODS OF PREVENTING OR TREATING INFLAMMATORY OR AUTOIMMUNE
: TITLE OF INVENTION: DISORDERS BY ADMINISTERING INTEGRIN ALPHA-V-BETA 3 ANTAGONISTS
: TITLE OF INVENTION: COMBINATION WITH OTHER PROPHYLACTIC OR THERAPEUTIC AGENTS
: FILE REFERENCE: 10271-053-999
: CURRENT APPLICATION NUMBER: US/10/091,236
: CURRENT FILING DATE: 2002-03-04
: PRIOR APPLICATION NUMBER: US 60/273,098
: PRIOR FILING DATE: 2001-03-02
: PRIOR APPLICATION NUMBER: US 60/316,321
: PRIOR FILING DATE: 2001-08-31
: NUMBER OF SEQ ID NOS: 17
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 15
: LENGTH: 7
: TYPE: PRT
: ORGANISM: Mus sp.
US-10-091-236-15

Query Match      60.0%; Score 3; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.7e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db      1 LES 4
      III
      5 LES 7

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Job time : 10 secs

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GenCore version 5.1.4-p5.4578
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OM protein - protein search, using sw model

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(without alignments)
9,543 Million cell updates/sec

Perfect score: 5
Sequence: 1 LEVST 5

Scoring table: CLIGO
Gapop 60.0, Gapext 60.0

Searched: 262574 seqs, 2042222 residues

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Local number of hits satisfying chosen parameters 77191

Minimum DB seq length: 0
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3 /cgm2_6/ptodata/1/iaa/6A-COMB-pep.*
4 /cgm2_6/ptodata/1/iaa/6B-COMB-pep.*
5 /cgm2_6/ptodata/1/iaa/PTUS-COMB-pep.*
6 /cgm2_6/ptodata/1/iaa/Backfiles-pep.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3	60.0	4	4	US-09-177-249-247
2	3	60.0	5	1	US-08-385-443-5
3	3	60.0	5	1	US-08-456-840-36
4	3	60.0	5	1	US-08-170-360-11
5	3	60.0	5	1	US-08-170-360-14
6	3	60.0	5	1	US-08-302-829-8
7	3	60.0	5	1	US-08-481-840A-6
8	3	60.0	5	1	US-08-266-407A-4
9	3	60.0	5	1	US-08-403-718-8
10	3	60.0	5	1	US-08-619-462-8
11	3	60.0	5	2	US-08-892-544-36
12	3	60.0	5	3	US-09-082-837A-8
13	3	60.0	5	4	US-09-421-845-8
14	3	60.0	5	4	US-09-298-924-35
15	3	60.0	5	6	5276016-4
16	3	60.0	5	6	5276016-8
17	3	60.0	5	6	5276016-10
18	3	60.0	5	6	5276016-11
19	3	60.0	6	1	US-07-853-2410-40
20	3	60.0	6	1	US-08-477-270-10
21	3	60.0	6	1	US-08-137-117D-10
22	3	60.0	6	2	US-08-436-717-10
23	3	60.0	6	2	US-08-436-063-3
24	3	60.0	6	2	US-08-702-673-4
25	3	60.0	6	2	US-08-893-853-44
26	3	60.0	6	2	US-08-310-912A-10
27	3	60.0	6	4	US-09-113-921-44

ALIGNMENTS

RESULT 1

US-09-177-249-247

: Sequence 247, Application US/99/177,249

: Patent No. 6229064

: GENERAL INFORMATION:

: APPLICANT: Fisher, Robert L.

: APPLICANT: Chad, Nir

: APPLICANT: Kiyosue, Tomohiro

: APPLICANT: Vagstad, Pamin

: APPLICANT: Margossian, Linda

: APPLICANT: Harada, John

: APPLICANT: Goldberg, Robert B.

: APPLICANT: The Regents of the University of California

: TITLE OF INVENTION: Nucleic Acids That Control Seed and Fruit

: TITLE OF INVENTION: Development in Plants

: FILE REFERENCE: 02070-08612005

: CURRENT APPLICATION NUMBER: US/99/177,249

: CURRENT FILING DATE: 1998-10-22

: EARLIER FILING DATE: 1998-05-01

: NUMBER OF SEQ ID NOS: 324

: SOFTWARE: Patent In Ver. 2.0

: SEQ ID NO 247

: LENGTH: 4

: TYPE: PRT

: ORGANISM: Arabidopsis sp.

: US-09-177-249-247

: Query Match

: Best Local Similarity 100.0%: Score 3, DB 4, Length 4:

: Matches 3: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

: QY 3 SYT 5

: DB 1 SYT 3

: RESULT 2

: US-09-395-443-5

: Sequence 5, Application US/98/35443

: Patent No. 5534495

: GENERAL INFORMATION:

: APPLICANT: FURT, CANDACE B.

: APPLICANT: RUFF, MICHAEL R.

: TITLE OF INVENTION: TREATMENT OF NON-HIV NEUROPATHIC

: NUMBER OF SEQUENCES: 6

: CORRESPONDENCE ADDRESS:

: ADDRESSEE: JULES E. GOLDBERG

: STREET: 261 MADISON AVENUE

Sequence 138, Appl
Sequence 139, Appl
Sequence 140, Appl
Sequence 141, Appl
Sequence 142, Appl
Sequence 143, Appl
Sequence 144, Appl
Sequence 145, Appl
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: CITY: NEW YORK
: STATE: NEW YORK
: COUNTRY: USA
: ZIP: 10016-2391
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.30
: CURRENT APPLICATION NUMBER: US/08/485,443
: FILING DATE: 08-FEB-1995
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 06/967,523
: FILING DATE: 23-MAY-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: GOLDBERG, JULES E.
: REGISTRATION NUMBER: 24,408
: REFERENCE/DOCKET NUMBER: ADVANCED PEPTIDE: P5
: TELEPHONE: 212-986-4090
: TELEFAX: 212-818-9479
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 5 amino acids
: TYPE: amino acid
: STRANDEDNESS: not relevant
: TOPOLOGY: not relevant
: MOLECULE TYPE: peptide
: US-08-385-443-5

Query Match 60.0% Score 3: DB 1: Length 5:
Best Local Similarity 100.0% Pred. No. 2e+05
Matches 3: Conservative 0: Mismatches 0: Indels 0:

QY 3 SYT 5
Db 3 SYT 5

RESULT 3
US-08-456-840-36
: Sequence 36, Application US/08456840
: Patent No. 5597908
: GENERAL INFORMATION:
: APPLICANT: Tadel-Peters, W. C.
: TITLE OF INVENTION: Immunoreactive Peptides of Apo(a)
: NUMBER OF SEQUENCES: 48
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Akzo No. 5597908el
: STREET: 1330 Piccard Drive
: CITY: Rockville
: STATE: Maryland
: COUNTRY: US
: ZIP: 20850
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/456,840
: FILING DATE: 01-JUN-1995
: CLASSIFICATION: 536
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/266,407
: FILING DATE: 27-JUN-1994
: APPLICATION NUMBER: US 08/172,461
: FILING DATE: 21-DEC-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: Gormley, Mary E.

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: REGISTRATION NUMBER: 34,409
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 301-258-5200
: TELEFAX: 301-977-0847
: INFORMATION FOR SEQ ID NO: 36:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 5 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-456-840-36

Query Match 60.0% Score 3: DB 1: Length 5:
Best Local Similarity 100.0% Pred. No. 2e+05
Matches 3: Conservative 0: Mismatches 0: Indels 0:

QY 1 LES 3
Db 1 LES 3

RESULT 4
US-08-170-360-11
: Sequence 11, Application US/08170360
: Patent No. 5656602
: GENERAL INFORMATION:
: APPLICANT: Tseng, Albert P. S.
: APPLICANT: Inglis, Adam
: TITLE OF INVENTION: PLAZ INHIBITORY COMPOUNDS
: NUMBER OF SEQUENCES: 17
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Rothwell, Figg Ernst & Kurz
: STREET: Suite 701-E, 555 Thirteenth St., N.W.
: CITY: Washington
: STATE: D.C.
: COUNTRY: U.S.A.
: ZIP: 20004
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/170,360
: FILING DATE: 03-MAR-1994
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: AU PRT/9002,00033
: FILING DATE: 06-JUL-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: AU PK 7058
: FILING DATE: 04-JUL-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Ernst, Barbara G.
: REGISTRATION NUMBER: 30,477
: REFERENCE/DOCKET NUMBER: 1871-104A
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202)783-6040
: TELEFAX: (202)783-6031
: INFORMATION FOR SEQ ID NO: 11:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 5 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: both
: MOLECULE TYPE: peptide
: HYPOTHETICAL: NO
: ANTI-SENSE: NO
: FRAGMENT TYPE: N-terminal
: US-08-170-360-11

Query Match 60.0% Score 3: DB 1: Length 5:
Best Local Similarity 100.0% Pred. No. 2e+05

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1  NUMBER OF SEQUENCES: 7
2  CORRESPONDENCE ADDRESS:
3  ADDRESSEE: Banner & Allegretti, Ltd.
4  STREET: 10 South Wacker Drive
5  CITY: Chicago
6  STATE: Illinois
7  COUNTRY: USA
8  ZIP: 60606
9
10 COMPUTER READABLE FORM:
11 MEDIUM TYPE: Floppy disk, 3.50 inch
12 COMPUTER: IBM PC compatible
13 OPERATING SYSTEM: MS-DOS
14 SOFTWARE: WordPerfect 6.1
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16 CURRENT APPLICATION DATA:
17 APPLICATION NUMBER: US/08/481 840A
18 FILING DATE: 07-JUN-1995
19 CLASSIFICATION: 514
20
21 PRIOR APPLICATION DATA:
22 APPLICATION NUMBER: 08/107,777
23 FILING DATE: 24-NOV-1993
24
25 ATTORNEY/AGENT INFORMATION:
26 NAME: Iwanicki, John P.
27 REGISTRATION NUMBER: 34,528
28 REFERENCE/DOCKET NUMBER: 93,741-A
29 TELECOMMUNICATION INFORMATION:
30 TELEPHONE: 617-345-9100
31 TELEFAX: 617-345-9111
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33 INFORMATION FOR SEQ ID NO. 6:
34 SEQUENCE CHARACTERISTICS:
35 LENGTH: 5 amino acids
36 TYPE: amino acid
37 STRANDEDNESS:
38 TOPOLOGY: Linear
39 MOLECULE TYPE: peptide
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41 US-08-481-840A-6
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44 Best Local Similarity 100.0%; Pred. No. 2e+05;
45 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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47 QY 3 SYT 5
48 III
49 DB 3 SYT 5
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51 RESULT 8
52 US-08-266-407A-36
53 Sequence 36, Application US/08266407A
54 Patent No. 5786156
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56 GENERAL INFORMATION:
57 APPLICANT: Tadel-Peters, W. C.
58 APPLICANT: Butler, Sandra M.
59 TITLE OF INVENTION: Immunoreactive Peptides of Apo(a)
60
61 NUMBER OF SEQUENCES: 48
62 CORRESPONDENCE ADDRESS:
63 ADDRESSEE: Akzo NO. 5786156el
64 STREET: 1330 Piccard Drive
65 CITY: Rockville
66 STATE: Maryland
67 COUNTRY: US
68 ZIP: 20850
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70 COMPUTER READABLE FORM:
71 MEDIUM TYPE: Floppy disk
72 COMPUTER: IBM PC compatible
73 OPERATING SYSTEM: PC-DOS/MS-DOS
74 SOFTWARE: PatentIn Release #1.0, Version #1.25
75 CURRENT APPLICATION DATA:
76 APPLICATION NUMBER: US/08/266,407A
77 FILING DATE: 27-JUN-1994
78 CLASSIFICATION: 435
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80 PRIOR APPLICATION DATA:
81 APPLICATION NUMBER: US 08/172,451
82 FILING DATE: 21-DEC-1993

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1  ATTORNEY/AGENT INFORMATION:
2  NAME: Goinley, Mary E.
3  REGISTRATION NUMBER: 34,409
4  TELECOMMUNICATION INFORMATION:
5  TELEPHONE: 301-258-5200
6  TELEFAX: 301-977-0847
7  INFORMATION FOR SEQ ID NO. 36:
8  SEQUENCE CHARACTERISTICS:
9  LENGTH: 5 amino acids
10 TYPE: amino acid
11 TOPOLOGY: linear
12 MOLECULE TYPE: protein
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14 US-08-266-407A-36
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16 Query Match 60.0%; Score 3; DB 1; Length 5;
17 Best Local Similarity 100.0%; Pred. No. 2e+05;
18 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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20 QY 1 LES 3
21 III
22 DB 1 LES 3
23
24 RESULT 9
25 US-08-403-718-8
26 Sequence 8, Application US/08403718
27 Patent No. 5795858
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29 GENERAL INFORMATION:
30 APPLICANT: MICHAELIS, JURGEN
31 APPLICANT: SUEIGH, MERILYN J.
32 TITLE OF INVENTION: TREATMENT OR PREVENTION OF CROHN'S
33 TITLE OF INVENTION: DISEASE AND/OR ULCERATIVE COLITIS
34 NUMBER OF SEQUENCES: 8
35 CORRESPONDENCE ADDRESS:
36 ADDRESSEE: NIXON & VANDERHYE P.C.
37 STREET: 1100 NORTH GLEBE ROAD
38 CITY: ARLINGTON
39 STATE: VIRGINIA
40 COUNTRY: U.S.A.
41 ZIP: 22201-4714
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44 MEDIUM TYPE: Floppy disk
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47 SOFTWARE: PatentIn Release #1.0, Version #1.30
48 CURRENT APPLICATION DATA:
49 APPLICATION NUMBER: US/08/403,718
50 FILING DATE: 31-MAR-1995
51 CLASSIFICATION: 514
52
53 ATTORNEY/AGENT INFORMATION:
54 NAME: MITCHELL, LEONARD C.
55 REGISTRATION NUMBER: 29,009
56 REFERENCE/DOCKET NUMBER: 47-74
57 TELECOMMUNICATION INFORMATION:
58 TELEPHONE: (703) 816-4000
59 TELEFAX: (704) 816-4100
60 INFORMATION FOR SEQ ID NO. -8:
61 SEQUENCE CHARACTERISTICS:
62 LENGTH: 5 amino acids
63 TYPE: amino acid
64 STRANDEDNESS:
65 TOPOLOGY: linear
66 MOLECULE TYPE: peptide
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68 US-08-403-718-8
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70 Query Match 60.0%; Score 3; DB 1; Length 5;
71 Best Local Similarity 100.0%; Pred. No. 2e+05;
72 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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74 QY 3 SYT 5
75 III
76 DB 3 SYT 5

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? GENERAL INFORMATION:
? APPLICANT: MICHAELIS, JURGEN
? APPLICANT: TRIGG, Timothy Elliot
? TITLE OF INVENTION: METHOD FOR THE TREATMENT OF PREVENTION OF
? TITLE OF INVENTION: EYEMETHEMATITIS
? NUMBER OF SEQUENCES: 8
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: NIXON & VANDEPHEVE P.C.
? STREET: 1100 NORTH GLEBE ROAD
? CITY: ARLINGTON
? STATE: VIRGINIA
? COUNTRY: U.S.A.
? ZIP: 22201-4734
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? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US-08-619-462
? FILING DATE: 07-MAY-1996
? CLASSIFICATION: 514
? ATTORNEY/AGENT INFORMATION:
? NAME: MITCHELL, LEONARD C.
? REGISTRATION NUMBER: 29,009
? REFERENCE/DOCKET NUMBER: 47-84
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (703) 816-4000
? TELEFAX: (703) 816-4100
? INFORMATION FOR SEQ ID NO: 8:
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? TOPOLOGY: linear
? MOLECULE TYPE: peptide
US-08-619-462-8

Query Match 60.0% Score 3 DB 1 Length 5;
Best Local Similarity 100.0% Pred. No. 2e-08
Matches 3, Conservative 0, Mismatches 0, Indels 0

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? Sequence 36, Application US/08892544
? Patent No. 5874544
? GENERAL INFORMATION:
? APPLICANT: Taddel-Peters, W. C.
? APPLICANT: Butler, Sandra M.
? TITLE OF INVENTION: Immunoreactive Peptides of Apo(a)
? NUMBER OF SEQUENCES: 48
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: ARA No. 5974544e1
? STREET: 1370 Piccard Drive
? CITY: Rockville
? STATE: Maryland
? COUNTRY: US
? ZIP: 20850
? COMPUTER READABLE FORM:
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? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patent In Release #1.0, Version #1.25

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? FILING DATE:
? CLASSIFICATION:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US-08-892-544
? FILING DATE: 27-JUN-1994
? APPLICATION NUMBER: US-08-892-544
? FILING DATE: 21-DEC-1993
? ATTORNEY/AGENT INFORMATION:
? NAME: Gormley, Mary E.
? REGISTRATION NUMBER: 34,409
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 301-258-5200
? TELEFAX: 301-977-0847
? INFORMATION FOR SEQ ID NO: 36:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 5 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
US-08-892-544-36

Query Match 60.0% Score 3 DB 2 Length 5;
Best Local Similarity 100.0% Pred. No. 2e-05
Matches 3, Conservative 0, Mismatches 0, Indels 0

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RESULT 12
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? Sequence 8, Application US/09082837A
? Patent No. 6011014
? GENERAL INFORMATION:
? APPLICANT: ANDERSEN, Anders J.
? APPLICANT: ASTON, Roger
? APPLICANT: CARLEN, Peter L.
? APPLICANT: DOUB, Penelope K.
? APPLICANT: MAGFADDEN, Douglas K.
? APPLICANT: PHIPPS, David J.
? APPLICANT: RATHJEN, Deborah
? APPLICANT: WIDMER, Fred
? TITLE OF INVENTION: Prolytic T and Related Peptides in the Treatment of
? TITLE OF INVENTION: Inflammation, Including Multiple Sclerosis
? NUMBER OF SEQUENCES: 11
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: BANNER & WITCOFF, LTD.
? STREET: 10 S. Wacker Drive
? CITY: Chicago
? STATE: Illinois
? COUNTRY: USA
? ZIP: 60606
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patent In Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US-09-082-837A
? FILING DATE: 21-JUN-1998
? CLASSIFICATION: 514
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US-08-892-544
? FILING DATE: 29-MAR-1993
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: WO-97/04464
? FILING DATE: 29-MAR-1993
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US-07-987-674
? FILING DATE: 09-DEC-1992

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Sequence 35, Application US/09/29/924
Patent No. 6391595
GENERAL INFORMATION:
APPLICANT: KATO, Masaru
MIURA, Yutaka
KETTOKU, Masako
IWAMATSU, Akihiro
KOBAYASHI, Kazuo
KOMEDA, Toshihiro
TITLE OF INVENTION: NOVEL TRANSFERASE AND AMYLASE, PROCESS
FOR PROTECTING THE ENZYMES, USE THEREOF, AND GENE CODING
FOR THE SAME
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 08/750,569
FILING DATE: 26-Apr-1999
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/750,569
FILING DATE: <unknown>
APPLICATION NUMBER: JP 7-120673
FILING DATE: 21-Apr-1995
APPLICATION NUMBER: JP 6-311185
FILING DATE: 21-Nov-1994
APPLICATION NUMBER: JP 6-286917
FILING DATE: 21-Nov-1994
APPLICATION NUMBER: JP 6-290394
FILING DATE: 31-Oct-1994
APPLICATION NUMBER: JP 6-194223
FILING DATE: 18-Aug-1994
APPLICATION NUMBER: JP 6-133354
FILING DATE: 16-Jun-1994
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/ATTORNEY NUMBER: 49441/110
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 35:
US-09-298-924-35
Query Match 60.0%, Score 3, DB 4, Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LES 3
DB 3 LES 5
RESULT 15
5276016-4
Patent No. 5276016

Prior Application Data:
APPLICATION NUMBER: US 07/915,118
FILING DATE: 17-Jul-1992
Prior Application Data:
APPLICATION NUMBER: DK 645/92
FILING DATE: 14-May-1992
Prior Application Data:
APPLICATION NUMBER: US 07/858,832
FILING DATE: 27-Mar-1992
ATTORNEY/AGENT INFORMATION:
NAME: Drethoff, W. Dennis
REGISTRATION NUMBER: 27193
REFERENCE/POCKET NUMBER: 94,772-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: both
MOLECULE TYPE: peptide
US-09-082-837A-8
Query Match 60.0%, Score 3, DB 3, Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 SYT 5
DB 3 SYT 5
RESULT 13
US-09-421-845-8
Sequence 8, Application US/09/421/845
Patent No. 6265374
GENERAL INFORMATION:
APPLICANT: Jorgensen
APPLICANT: Aston
APPLICANT: Carlen
APPLICANT: Ewob
APPLICANT: MacFadden
APPLICANT: Phipps
APPLICANT: Rathjen
APPLICANT: Wadmer
TITLE OF INVENTION: Peptide I and Related Peptides In the Treatment of
TITLE OF INVENTION: Inflammation, Including Multiple Sclerosis.
FILE REFERENCE: Peptide I Inflammation
CURRENT APPLICATION NUMBER: US/09/421/845
CURRENT FILING DATE: 1999-10-20
Prior Application Number: 09/082,837
Prior Filing Date: 1998-05-21
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 8
LENGTH: 5
TYPE: PRI
ORGANISM: Homo sapiens
US-09-421-845-8
Query Match 60.0%, Score 3, DB 4, Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 SYT 5
DB 3 SYT 5
RESULT 14
US-09-298-924-35

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: APPLICANT: PERT, CANDACE B.; RUFF, WILLIAM F.
: FARRAR, WILLIAM L.
: TITLE OF INVENTION: SMALL PEPTIDES WHICH INHIBIT
: BINDING TO T-4 RECEPTORS AND ACT AS IMMUNOGENS
: NUMBER OF SEQUENCES: 19
: CURRENT APPLICATION DATA:
:   APPLICATION NUMBER: US 07,669,616
:   FILING DATE: 16-AUG-1990
: PRIOR APPLICATION DATA:
:   APPLICATION NUMBER: 314,507
:   FILING DATE: 15-FEB-1989
: APPLICATION NUMBER: 48,148
: FILING DATE: 11-MAY-1987
: APPLICATION NUMBER: 878,585
: FILING DATE: 26-JUN-1986
: APPLICATION NUMBER: 869,919
: FILING DATE: 03-JUN-1986
: SEQ ID NO: 4
: LENGTH: 5
: 526016-4
:
: any Match          60.0%; Score 3; DB 6; Length 5;
: best Local Similarity 100.0%; Pred. No. 2e+05;
: Matches 3; Conservative 0; Mismatches 0; Gaps 3;
:
: QY      3 SYT 5
: BB      3 SYT 5
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Search completed: April 29, 2003, 09:55:02
Job time : 17.4167 secs

GenCore version 5.1.4.10.4578
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OM protein - protein search, using sw model

Run on: April 29, 2003, 08:50:15 : Search time 21 5833 Seconds
(without alignments)
9,543 Million cell updates/sec

Title: US-09-647-749A-2

Perfect score: 7
Sequence: 1 KEYWORDS 7

Scoring table: GCGO
Gapop 60.0 : Gapext 60.0

Searched: 262574 seqs, 29422922 residues

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Total number of hits satisfying chosen parameters: 77191

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: listing first 45 summaries

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4: /gmo_6/prodata/1/aa/5D-CMB.pep*
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6: /gmo_6/prodata/1/aa/5F-CMB.pep*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	4	57.1	9	5	PCT-US95-16415-34
3	4	57.1	10	4	US-09-187-859-2791
4	3	42.9	4	1	US-08-416-007-3
5	3	42.9	4	2	US-08-475-251-3
6	3	42.9	5	1	US-08-244-846-3
7	3	42.9	5	1	US-08-737-757-3
8	3	42.9	5	2	US-08-574-959A-11
9	3	42.9	5	2	US-08-412-016-7
10	3	42.9	5	2	US-08-684-594-7
11	3	42.9	5	3	US-08-593-740-42
12	3	42.9	5	3	US-08-486-141A-71
13	3	42.9	5	3	US-08-469-141A-71
14	3	42.9	5	4	US-08-591-632-24
15	3	42.9	5	4	US-08-109-879-47
16	3	42.9	5	4	US-09-357-014-11
17	3	42.9	5	4	US-09-267-921-1
18	3	42.9	4	4	US-09-611-451-24
19	3	42.9	5	4	US-08-306-542A-64
20	3	42.9	5	5	PCT-US95-13794-71
21	3	42.9	5	5	PCT-US95-13794-71
22	4	42.9	6	1	US-08-297-731-4
23	3	42.9	6	1	US-08-290-448A-41
24	3	42.9	6	1	US-08-290-448A-41
25	3	42.9	6	1	US-08-175-069A-41
26	3	42.9	6	2	US-08-528-523-4
27	3	42.9	6	4	US-08-893-654B-15

28 3 42.9 6 4 US-09-442-271-28
29 3 42.9 6 4 US-09-623-618B-6
30 3 42.9 6 4 US-08-461-979A-41
31 3 42.9 6 4 US-08-464-000-41
32 3 42.9 6 4 US-09-556-605-52
33 3 42.9 6 5 PCT-US95-10793-4
34 3 42.9 6 6 518642-7
35 3 42.9 6 6 510657-19
36 3 42.9 7 1 US-08-137-614A-31
37 3 42.9 7 1 US-09-297-731-5
38 3 42.9 7 1 US-07-942-245-500
39 3 42.9 7 2 US-08-317-310A-18
40 3 42.9 7 4 US-09-623-618B-7
41 3 42.9 7 4 US-09-187-859-457
42 3 42.9 7 4 US-09-187-859-3047
43 3 42.9 7 4 US-09-456-605-51
44 3 42.9 7 5 PCT-US95-10793-5
45 3 42.9 7 5 PCT-US95-14041-18

ALIGNMENTS

RESULT 1
US-09-187-859-2791
Sequence 2791, Application US/69187859A
Patent No. 6358920
GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: COMPLEXES AND METHODS FOR MUTATION NON-CLASSICAL
TITLE OF INVENTION: CACHEIN-MEDIATED FUNCTIONS
FILE REFERENCE: 1,000,470C1
CURRENT APPLICATION NUMBER: US 09-187,859A
CURRENT FILING DATE: 1998-11-06
PRIORITY OF SEQ. NO. 4952
SOFTWARE: PatentIn Ver. 2.0
SEQ. ID NO. 2791
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Representative cyclic modulation agent based ch.
OTHER INFORMATION: Protocadherin cell adhesion recognition sequence
US-09-187-859-2791

Query Match 57.1% Score 4: DB 4: Length 9:
Best Local Similarity 100.0% Pred. No. 2e+05:
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

Qy 3 EYFT 5
Db 1 EYFT 4

RESULT 2
PCT-US95-16415-34
Patent No. 41, Application No. 1991-09516415
GENERAL INFORMATION:
APPLICANT: The Scripps Research Institute
TITLE OF INVENTION: IN VIVO ACTIVATION OF TWEET-SPECIFIC
TITLE OF INVENTION: CYTOTOXIC T CELLS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESS: The Scripps Research Institute
STREET: 10550 North Torrey Pines Road, IPC-9
CITY: La Jolla
STATE: California
COUNTRY: US
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/16415
 FILING DATE: 13-DEC-1995
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/355,558
 FILING DATE: 14-DEC-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Logan, April C.
 REGISTRATION NUMBER: 33,950
 REFERENCE/DOCKET NUMBER: 433 IPC
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 554-2937
 TELEFAX: (619) 554-6412
 INFORMATION FOR SEQ ID NO: 34:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: heptade
 PCT-US95-16415-34

Query Match 57.1%, Score 4, DB 4, Length 10;
 Best Local Similarity 100.0%, Pred. No. 2e-05;
 Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EYFT 6
 DB 5 EYFT 8

RESULT 3
 US-09-187-859-2792
 Sequence 3, Application US/09187859A
 Patent No. 6358920
 GENERAL INFORMATION:
 APPLICANT: Blaschuk, Orest W.
 APPLICANT: Gour, Barbara J.
 TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MEDIATING NONCLASSICAL
 TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
 FILE REFERENCE: 100086.407C1
 CURRENT APPLICATION NUMBER: US/09/187.859A
 CURRENT FILING DATE: 1998-11-06
 NUMBER OF SEQ ID NOS: 4052
 SOFTWARE: Patent In Ver. 2.0
 SEQ ID NO 2792
 LENGTH: 10
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Representing cyclic amino acid based on
 OTHER INFORMATION: Protocadherin cell adhesion recognition sequence
 US-09-187-859-2792

Query Match 57.1%, Score 4, DB 4, Length 10;
 Best Local Similarity 100.0%, Pred. No. 1e-05;
 Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EYFT 6
 DB 1 EYFT 4

RESULT 4
 US-08-416-007-3
 Sequence 3, Application US/08416007
 Patent No. 5693679
 GENERAL INFORMATION:
 APPLICANT: Vincent, Jean-Pierre
 APPLICANT: Gaudriault, Georges
 APPLICANT: Beaudet, Alain

TITLE OF INVENTION: FLUORESCENT SOMATOSTATIN
 NUMBER OF SEQUENCES: 5
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson P.C.
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02110-2804
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/416.007
 FILING DATE: 04-APR-1995
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Clark, Paul T.
 REGISTRATION NUMBER: 30,162
 REFERENCE/DOCKET NUMBER: 06942/000001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617/542-5070
 TELEFAX: 617/542-8906
 TELEX: 200154
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-416-007-3

Query Match 42.9%, Score 3, DB 1, Length 4;
 Best Local Similarity 100.0%, Pred. No. 2e-05;
 Matches 3: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FTS 7
 DB 1 FTS 3

RESULT 5
 US-08-475-751-4
 Sequence 3, Application US/08475751
 Patent No. 5824772
 GENERAL INFORMATION:
 APPLICANT: Vincent, Jean-Pierre
 APPLICANT: Gaudriault, Georges
 APPLICANT: Beaudet, Alain
 TITLE OF INVENTION: FLUORESCENT SOMATOSTATIN
 NUMBER OF SEQUENCES: 5
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Clark & Elbing LLP
 STREET: 585 Commercial Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109-1024
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/475.751
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/416.007
 FILING DATE: 04-APR-1995

ATTORNEY/AGENT INFORMATION:
 NAME: Clark, Paul T.
 REGISTRATION NUMBER: 30,162
 REFERENCE/DOCKET NUMBER: 06942/004001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617/723-4123
 TELEFAX: 617/723-8462
 TELEX:
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-475-751-3

Query Match 42.9% Score 3; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+05; 0;
 Matches 3; Conservative 0; Mismatches 0; Indels 0;

QY 5 FTS 7
 III
 Ib 1 FTS 3

RESULT 6
 US-08-244-646-3
 ; Sequence 3, Application US/08244646
 ; Patent No. 5744692
 ; GENERAL INFORMATION:
 ; APPLICANT: Ceryone, Felice
 ; APPLICANT: De Lorenzo, Giulia
 ; APPLICANT: Salvi, Giovanni
 ; APPLICANT: Albersheim, Peter
 ; APPLICANT: Darvill, Alan
 ; APPLICANT: Bergmann, Carl
 ; TITLE OF INVENTION: Nucleotide Sequences Coding An
 ; TITLE OF INVENTION: Endopolygalacturonase Inhibitor
 ; NUMBER OF SEQUENCES: 17
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Sally A. Sullivan
 ; STREET: 5470 Manhattan Circle Suite 201
 ; CITY: Boulder
 ; STATE: CO
 ; COUNTRY: US
 ; ZIP: 80403
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-PCS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US 08 144 646
 ; FILING DATE: 06-JUN-1994
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: IT PM 91A 000915
 ; FILING DATE: 06-DEC-1991
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: WO PCT/IT/00158
 ; FILING DATE: 04-DEC-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Sullivan, Sally A.
 ; REGISTRATION NUMBER: 32,054
 ; REFERENCE/DOCKET NUMBER: 19-94
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (303)499-8090
 ; TELEFAX: (303)499-9090
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 5 amino acids
 ; TYPE: amino acid

STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Plasmodium vulgaris
 STRAIN: Pinto
 US-08-244-646-3

Query Match 42.9% Score 3; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2e+05; 0;
 Matches 3; Conservative 0; Mismatches 0; Indels 0;

QY 5 FTS 7
 III
 Db 2 FTS 4

RESULT 7
 US-08-737-757-3
 ; Sequence 3, Application US/08737757
 ; Patent No. 5783413
 ; GENERAL INFORMATION:
 ; APPLICANT: Pedersen, John
 ; APPLICANT: Lauritzen, Conni
 ; APPLICANT: Madsen, Mads Thorup
 ; TITLE OF INVENTION: An enzymatic process for
 ; TITLE OF INVENTION: Producing a desired protein from an amino acid
 ; TITLE OF INVENTION: protein
 ; NUMBER OF SEQUENCES: 17
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Darby & Darby, PC
 ; STREET: 805 Third Avenue - 27th floor
 ; CITY: New York
 ; STATE: NY
 ; COUNTRY: USA
 ; ZIP: 10022-7513
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US 08 737,757
 ; FILING DATE: 05-FEB-1997
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: GOGORIS, Anna C
 ; REGISTRATION NUMBER: 29,714
 ; REFERENCE/DOCKET NUMBER: 4-97, 06596
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212-522-7700
 ; TELEFAX: 212-751-6237
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 5 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-737-757-3

Query Match 42.9% Score 3; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2e+05; 0;
 Matches 3; Conservative 0; Mismatches 0; Indels 0;

QY 5 FTS 7
 III


```

PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 08/143,903
  FILING DATE: 02-NOV-1993
  ATTORNEY/AGENT INFORMATION:
    NAME: WILSON, MAPY J
    REGISTRATION NUMBER: 32,955
    REFERENCE/DOCKET NUMBER: 1579-112
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: (703) 816-4000
    TELEFAX: (703) 816-4100
  INFORMATION FOR SEQ ID NO: 7:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 5 amino acids
      TYPE: amino acid
      STRANDEDNESS:
      TOPOLOGY: linear
    MOLECULE TYPE: protein
  US-08-584-594-7

Query Match 42.9%, Score 3; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e-05;
Matches 3; Conservative 0; Mismatches 0; Indels 0;

QY 1 IKE 3
Db 1 IKE 3

RESULT 11
US-08-582-740-42
  Sequence 42, Application US/08/02740
  Patent No. 6037324
  GENERAL INFORMATION:
    APPLICANT: Schwender, Charles F.
    APPLICANT: Shroff, Hitesh N.
    TITLE OF INVENTION: Inhibitors of MadCAM-1-Mediated
    TITLE OF INVENTION: Interactions and Methods of Use Therefor
    NUMBER OF SEQUENCES: 70
    CORRESPONDENCE ADDRESS:
      ADDRESSEE: Hamilton Brook Smith & P-200 Ltd. P. O.
      STREET: Two Militia Drive
      CITY: Lexington
      STATE: Massachusetts
      COUNTRY: USA
      ZIP: 02173
    COMPUTER READABLE FORM:
      MEDIUM TYPE: Floppy disk
      COMPUTER: IBM PC compatible
      OPERATING SYSTEM: PC-DOS/MS-DOS
      SOFTWARE: Patent In Release #1.0, Version #1.0
    CURRENT APPLICATION DATA:
      APPLICATION NUMBER: US/08-582-740
      FILING DATE: 04-JAN-1996
      CLASSIFICATION: 514
    ATTORNEY/AGENT INFORMATION:
      NAME: Brook, David E.
      REGISTRATION NUMBER: 22,592
      REFERENCE/DOCKET NUMBER: LKS95-12
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: (617) 861-6240
    TELEFAX: (617) 861-9540
  INFORMATION FOR SEQ ID NO: 42:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 5 amino acids
      TYPE: amino acid
      STRANDEDNESS:
      TOPOLOGY: linear
    MOLECULE TYPE: peptide
  FEATURE:
    NAME/KEY: Modified-site
    LOCATION: 1
    OTHER INFORMATION: /label=modified aa
    OTHER INFORMATION: /note="Ac - Leucine"

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FEATURE:
  NAME/KEY: Modified-site
  LOCATION: 5
  OTHER INFORMATION: /label=modified aa
  OTHER INFORMATION: /note="Leucine - RH2"
  US-08-582-740-42

Query Match 42.9%, Score 3; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e-05;
Matches 3; Conservative 0; Mismatches 0; Indels 0;

QY 5 FTS 7
Db 2 FTS 4

RESULT 12
US-08-469-141A-20
  Sequence 20, Application US/08/469141A
  Patent No. 6124107
  GENERAL INFORMATION:
    APPLICANT: HOFFER, RICHARD A.
    APPLICANT: DAVIES, D.T. PHILIP
    APPLICANT: DAHLGREN, MARY E.
    APPLICANT: RAGER, JOSHUA S.
    APPLICANT: HUNES, JOHN L.
    TITLE OF INVENTION: ASSAY FOR MARKER OF HUMAN
    TITLE OF INVENTION: POLYMERHORMONAL CLEAR LEUKOCYTE ELASTASE ACTIVITY
    NUMBER OF SEQUENCES: 71
    CORRESPONDENCE ADDRESS:
      ADDRESSEE: RE. CHRISTINE E. CARTY
      STREET: 124 E. LINCOLN AVENUE, P.O. BOX 2000
      CITY: RABRAY
      STATE: NEW JERSEY
      COUNTRY: USA
      ZIP: 07065-0907
    COMPUTER READABLE FORM:
      MEDIUM TYPE: Floppy disk
      COMPUTER: IBM PC compatible
      OPERATING SYSTEM: PC-DOS/MS-DOS
      SOFTWARE: Patent In Release #1.0, Version #1.30
    CURRENT APPLICATION DATA:
      APPLICATION NUMBER: US/08/469,141A
      FILING DATE: 06-JUN-1995
      CLASSIFICATION: 435
    ATTORNEY/AGENT INFORMATION:
      NAME: CARTY, CHRISTINE E.
      REGISTRATION NUMBER: 36,099
      REFERENCE/DOCKET NUMBER: 174611B
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: (908)-594-5734
    TELEFAX: (908)-594-4720
  INFORMATION FOR SEQ ID NO: 20:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 5 amino acids
      TYPE: amino acid
      STRANDEDNESS: single
      TOPOLOGY: linear
      MOLECULE TYPE: peptide
      HYPOTHETICAL: NO
      ANTI-SENSE: NO
      FRAGMENT TYPE: internal
  US-08-469-141A-20

Query Match 42.9%, Score 3; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e-05;
Matches 3; Conservative 0; Mismatches 0; Indels 0;

QY 5 FTS 7
Db 1 FTS 3

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RESULT 14
US-08-469-141A-71
Sequence 71, Application US/08469141A
Patent No. 6124107
GENERAL INFORMATION:
APPLICANT: MONFORD, RICHARD A.
APPLICANT: DAVIES, D.T. PHILIP
APPLICANT: DAHLGREN, MARY E.
APPLICANT: BOGER, JOSHUA S.
APPLICANT: HOMES, JOHN L.
TITLE OF INVENTION: ASSAY FOR MARKER OF HUMAN
POLYMORPHONUCLEAR LEUKOCYTE ELASTASE ACTIVITY
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSEE: DR. CHRISTINE E. CARTY
STREET: 126 E. LINCOLN AVENUE., P.O. BOX 2009
CITY: RAHWAY
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,141A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CARTY, CHRISTINE E.
REGISTRATION NUMBER: 36,099
REFERENCE/DOCKET NUMBER: 174611B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)-594-6734
TELEFAX: (908)-594-4720
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
US-08-469-141A-71
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Best Local Similarity 100.0%, Pred. No. 2e+05,
Matches 3, Conservative 0, Mismatches 0, Indels 0, Gaps 0:
QY 5 FTS 7
Db 1 FTS 3
RESULT 14
US-08-591-632-24
Sequence 24, Application US/08591632
Patent No. 6261558
GENERAL INFORMATION:
APPLICANT: Barbas, Carlos F.
APPLICANT: Burton, Dennis R.
APPLICANT: Leifer, Richard A.
TITLE OF INVENTION: SYNTHETIC HUMAN NEUTRALIZING MONOCLONAL
ANTIBODIES TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 92
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10550 No. 6261558th Torrey Pines Road, TPC 8
CITY: La Jolla

STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/691,632
FILING DATE: 19-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/11907
FILING DATE: 19-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/208,841
FILING DATE: 19-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/233,619
FILING DATE: 26-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/139,409
FILING DATE: 19-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSHI 332.3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 784-9399
TELEFAX: (619) 784-2937
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-591-632-24
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Matches 3, Conservative 0, Mismatches 0, Indels 0, Gaps 0:
QY 4 YFT 6
Db 1 YFT 3
RESULT 15
US-09-109-879-42
Sequence 42, Application US/09109879
Patent No. 6274556
GENERAL INFORMATION:
APPLICANT: Schwender, Charles F.
APPLICANT: Shroff, Hitesh N.
TITLE OF INVENTION: INHIBITORS OF HADGAM-1-MEDIATED
INTERACTIONS AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
ZIP: 02421
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/109,879
FILING DATE: 02-JUL-1998
CLASSIFICATION: 514

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PRIOR APPLICATION DATA:
  APPLICATION NUMBER: PCT/US97/00291
  FILING DATE: 03-JAN-1997
PRIOR APPLICATION DATA: US 08/582,740
  APPLICATION NUMBER: US 08/582,740
  FILING DATE: 04-JAN-1996
  ATTORNEY/AGENT INFORMATION:
    NAME: BROOK, David E.
  REGISTRATION NUMBER: 22,592
  REFERENCE/DOCKET NUMBER: LKS95-12A2
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: (781) 861-6240
    TELEFAX: (781) 861-9540
  INFORMATION FOR SEQ ID NO: 42:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 5 amino acids
      TYPE: amino acid
      STRANDEDNESS:
      TOPOLOGY: linear
      MOLECULE TYPE: peptide
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        NAME/KEY: Modified-site
        LOCATION: 1
        OTHER INFORMATION: /label= modified aa
        OTHER INFORMATION: /note= "Ac - Leucine"
      FEATURE:
        NAME/KEY: Modified-site
        LOCATION: 5
        OTHER INFORMATION: /label= modified aa
        OTHER INFORMATION: /note= "Leucine - NH2"
US-09-109-879-42

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Best Local Similarity 100.0%  Pred. No. 2e-05;
Matches  4;  Conservatv  0;  Mismatches  0;  Indels  0;  Gaps  0;

QY  5 FTS 7
DB  2 FTS 4

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Search completed: April 29, 2003, 08:55:04
 Job time : 23.5833 secs

GenCore version 5.1.4.1_4578
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OM protein - protein search, using SW model

Run on: April 29, 2003, 09:06:29 - Search time: 37.4157 seconds

(without alignments)
52,508 Million cell updates/sec

Title: US-09-647-749A-2

Perfect score: 7 IKEYFTS 7

Sequence: 1 IKEYFTS 7

Scoring table: OLIGO
Gapop 50.0, Gapext 50.0

Searched: 671588 seqs, 206047115 residues

Word size: 6

Total number of hits satisfying cheson parameters: 1224

Minimum DB seq length: 0

Maximum DB seq length: 10

Post-processing: Listing first 45 summaries

Database:

SPTREML-21: *
1: sp_archaea: *
2: sp_bacteria: *
3: sp_fungi: *
4: sp_human: *
5: sp_invertebrate: *
6: sp_mammal: *
7: sp_mhc: *
8: sp_orquanelle: *
9: sp_phage: *
10: sp_plant: *
11: sp_rodent: *
12: sp_virus: *
13: sp_vertebrate: *
14: sp_unclassified: *
15: sp_virus: *
16: sp_bacteriophage: *
17: sp_archaea: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3	42.9	9	Q9N6M5	Q9N6M5 toxoplasma
2	3	42.9	10	Q934S1	Q934S1 thermus the
3	3	42.9	10	Q9NP07	Q9NP07 homo sapien
4	3	42.9	10	Q9N6M6	Q9N6M6 homo sapien
5	2	28.6	7	P72091	P72091 nocardia la
6	2	28.6	8	Q9S6D5	Q9S6D5 escherichia
7	2	28.6	8	Q9P7T2	Q9P7T2 escherichia
8	2	28.6	4	Q9P4S0	Q9P4S0 bacillus su
9	2	28.6	8	Q55759	Q55759 xanthobacte
10	2	28.6	8	P77556	P77556 escherichia
11	2	28.6	8	Q8R3T0	Q8R3T0 streptomyce
12	2	28.6	8	P87125	P87125 saccharomye
13	2	28.6	8	Q9H4D3	Q9H4D3 homo sapien
14	2	28.6	8	Q15888	Q15888 homo sapien
15	2	28.6	8	Q15893	Q15893 homo sapien
16	2	28.6	8	Q8TF70	Q8TF70 homo sapien

17	2	28.6	8	6	Q18854	Q18854 canis fami
18	2	28.6	8	6	Q95M23	Q95M23 sus scrofa
19	2	28.6	8	7	Q29610	Q29610 homo sapien
20	2	28.6	8	8	Q942E5	Q942E5 leptospermu
21	2	28.6	9	9	Q34209	Q34209 locusta mig
22	2	28.6	8	8	Q94VE6	Q94VE6 varanus job
23	2	28.6	8	10	Q9SAY7	Q9SAY7 discoborea t
24	2	28.6	8	11	Q9ET21	Q9ET21 mus musculu
25	2	28.6	8	11	Q8KSM9	Q8KSM9 mus musculu
26	2	28.6	8	12	Q84273	Q84273 human papil
27	2	28.6	8	12	Q84332	Q84332 murine hepa
28	2	28.6	9	2	Q9R9C4	Q9R9C4 borrelia bo
29	2	28.6	9	2	Q51349	Q51349 pseudomonas
30	2	28.6	9	2	Q93E20	Q93E20 streptococ
31	2	28.6	9	4	Q9HY19	Q9HY19 homo sapien
32	2	28.6	9	4	Q9H4R1	Q9H4R1 homo sapien
33	2	28.6	9	4	Q15891	Q15891 homo sapien
34	2	28.6	9	4	P78484	P78484 homo sapien
35	2	28.6	9	4	Q14277	Q14277 homo sapien
36	2	28.6	9	4	Q9U6W0	Q9U6W0 homo sapien
37	2	28.6	9	4	Q96P97	Q96P97 homo sapien
38	2	28.6	9	4	Q9UGF4	Q9UGF4 homo sapien
39	2	28.6	9	9	Q9TKC1	Q9TKC1 calothamnu
40	2	28.6	9	8	Q9TKF2	Q9TKF2 asteromytu
41	2	28.6	9	8	Q9MMG9	Q9MMG9 bateo bateo
42	2	28.6	9	8	Q9MMF4	Q9MMF4 bateo rufin
43	2	28.6	9	8	Q94V10	Q94V10 varanus dry
44	2	28.6	9	8	Q8W3E6	Q8W3E6 procladius
45	2	28.6	9	11	Q9QVH9	Q9QVH9 mus sp. sup

ALIGNMENTS

RESULT 1
Q9N6M5 PRELIMINARY: PPI: R AA.
AC Q9N6M5:
DT 01-OCT-2000 (TREMREL: 15, Created)
DT 01-OCT-2000 (TREMREL: 15, Last sequence update)
DT 01-OCT-2000 (TREMREL: 15, Last annotation update)
DE Dihydrofolate reductase thymidylate synthase (Fragment).
GN Foli.
OS Toxoplasma gondii.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Sarcocystidae;
OC Toxoplasma.
OX NCBI_TaxID=5811;
RN [1]
RF SEQUENCE FROM N.A.
RT STRAIN:5H, CM33AF, T755134, SEA OTTER TC828G1, AND BEVERLEY;
RA Lehmann T., Plaverson C.R., Farmlay S.F., Remington J.S., Burey J.P.;
RT "Strain Typing of Toxoplasma gondii: Comparison of Antigen-Coding and
Housekeeping Genes."
RL J. Parasitol., 0:0-0(2000).
DR EMBL: AF249695; AAF79151.1; -
DR EMBL: AF249692; AAF79150.1; -
DR EMBL: AF249693; AAF79151.1; -
DR EMBL: AF219541; AAF79151.1; -
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA, 1005 MW, 136000AAACEE133044 Q5064;
Query Match 42.9%; Score 3; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 6 70-05;
Matches 10 Conservative 0; Mismatches 0; Gaps 0;
QY 1 IWE 3
LQ 2 IPE 4
RESULT 2
Q934S1

DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
 DE Putative IS30 transposase (Fragment).
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision: Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxID=562.
 RN [1]
 PP SEQUENCE FROM N.A.
 RC STRAIN=A295B;
 RX MEDLINE=99194747; PubMed=10094716;
 RA Rahn A., Drummel-Smith J., Whitfield C.
 RT "Conserved organization in the cps gene clusters for expression of
 Escherichia coli group 1 K antigens: relationship to the colicin *aciB*
 RT biosynthesis locus and the cps genes from *Klebsiella pneumoniae*."
 RL J. Bacteriol. 181:2307-2311(1999).
 DR EMBL: AF118251; AAD30008.1;
 FT NON_TER 8
 SQ SEQUENCE 8 AA; 1011 MW; F21DC1A3D1B41406 (RC64);

Query Match 28.6%, Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 6.7e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FT 6
 II
 DB 5 FT 6

RESULT 7

Q9R7T2
 ID Q9R7T2 PRELIMINARY; PRT; 8 AA.
 AC Q9R7T2
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 13, Last annotation update)
 DE Hypothetical 1.0 kDa protein (Fragment).
 GN Y0FG.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision: Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 PP SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE=97061202; PubMed=9905242;
 RA Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
 RA Ikenoto K., Inada T., Itoh T., Kajihara M., Kawai K., Kashimoto K.,
 RA Kimura S., Kiradawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
 RA Mori H., Motomura K., Nakamura Y., Nashimura H., Nishio Y., Saito N.,
 RA Sempel G., Seki Y., Tagami H., Takenoto K., Wada C., Yamamoto Y.,
 RA Yano M., Horiuchi T.;
 RT "A 718-kb DNA Sequence of Escherichia coli K-12 Genome Corresponding
 RT to the 12,738,000-bp Region on the Linkage Map";
 RL DNA Res. 3:117-155(1996).
 DR EMBL: D90705; BAA35310.1;
 KW Hypothetical protein.
 FT NON_TER 1
 SQ SEQUENCE 8 AA; 914 MW; FE13B81DD04B476A (RC64);

Query Match 28.6%, Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 6.7e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KE 3
 II
 DB 7 KE 8

RESULT 8

Q9R9E0
 ID Q9R9E0 PRELIMINARY; PRT; 8 AA.
 AC Q9R9E0
 DT 01-MAY-2000 (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
 GN SPOVE.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillus/Clustidium group; Bacillales;
 OC Bacillaceae; Bacillus.
 OX NCBI_TaxID=1423;
 RN [1]
 PP SEQUENCE FROM N.A.
 RC STRAIN=168;
 PX MEDLINE=99001520; PubMed=1391053;
 RA Henriques A. O., de Lencastre H., Piggot P. J.;
 RT "A Bacillus subtilis morphogene cluster that includes *spoVE* is
 RT involved in the sporulation of *Escherichia coli*."
 RL Biochimie 74:735-748(1992).
 DR EMBL: X64258; CAA45556.1;
 FT NON_TER 8
 SQ SEQUENCE 8 AA; 893 MW; EE75A1A13321B1A6 (RC64);

Query Match 28.6%, Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 6.7e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 IS 7
 II
 DB 6 IS 7

RESULT 9

Q56759
 ID Q56759 PRELIMINARY; PRT; 8 AA.
 AC Q56759
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Halocacid dehalogenase (Fragment).
 GN DHLB.
 OS Xanthobacter autotrophicus.
 OC Bacteria; Proteobacteria; alpha subdivision: Rhizobiaceae group;
 OC Hyphomicrobium group; Xanthobacter.
 OX NCBI_TaxID=280;
 RN [1]
 PP SEQUENCE FROM N.A.
 RC STRAIN=GJ10; AND CV. MS0;
 RX MEDLINE=9517113; PubMed=7666610;
 RA Van der Ploeg J., Willemse M., van Hall G., Janssen D.B.;
 RT "Adaptation of Xanthobacter autotrophicus GJ10 to bromoacetate due to
 RT activation and mobilization of the haloacetate dehalogenase gene by
 RT insertion element IS1247";
 RL J. Bacteriol. 177:1348-1356(1995).
 DR EMBL: X84018; CAA58857.1;
 FT NON_TER 8
 SQ SEQUENCE 8 AA; 922 MW; F1A9D2D2DD31056 (RC64);

Query Match 29.6%, Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 6.7e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IK 2
 II
 DB 2 IK 3

RESULT 10

P77556
 ID P77556 PRELIMINARY; PRT; 8 AA.
 AC P77556
 DT 01-FEB-1997 (TREMBlrel. 02, Created)
 DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)
 DT 01-JAN-1999 (TREMBlrel. 09, Last annotation update)
 DE TRAY (Fragment).
 GN TRAY.

```

OS Escherichia coli.
OG Plasmid IncFII fl.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ECOR11;
RC MEDLINE=96400906; PubMed=8807284;
RA Boyd E.F., Hill C.W., Rich S.M., Hartl D.L.
RT "Mosaic structure of plasmids from natural populations of Escherichia
colii".
RL Genetics 143:1061-1100(1996).
DR EMBL: U50661; AAC44245.1; -
DR EMBL: U50650; AAC44234.1; -
DR EMBL: U50651; AAC44235.1; -
DR EMBL: U50652; AAC44236.1; -
DR EMBL: U50653; AAC44237.1; -
DR EMBL: U50654; AAC44238.1; -
DR EMBL: U50655; AAC44239.1; -
DR EMBL: U50656; AAC44240.1; -
DR EMBL: U50657; AAC44241.1; -
DR EMBL: U50658; AAC44242.1; -
DR EMBL: U50659; AAC44243.1; -
DR EMBL: U50660; AAC44244.1; -
KW Plasmid.
FT NON_TER 1 1
SQ SEQUENCE 8 AA: 834 MW: D335A5B0544735A1 CF 64:

Query Match 28.6%; Score 2; DB 2; length 8;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TS 7
DB 1 TS 2

RESULT 11
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AC Q8RJ10;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE DNA replication initiation protein (Fragment).
GN DNAA-LIKE.
OS Streptomyces caespitosus.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomycetes.
OX NCBI_TaxID=53502;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC27422.
RA Ma W., Mac X., Jie L., Qin Z.J., Jiang W.H., Zhao B.S., Zhao G.P.
RT "Cloning, sequence analysis and function analysis of the replication
origin oriC of Streptomyces albidus DSM 12227".
RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ458440; CAD30324.1; -
FT NON_TER 1 1
SQ SEQUENCE 8 AA: 915 MW: 04744535440451A7 CF 64:

Query Match 28.6%; Score 2; DB 2; length 8;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IK 2
DB 5 IK 6

RESULT 12
P87225

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ID P87225 PRELIMINARY: PRT: 8 AA.
AC P87225;
DT 01-MAY-1997 (TrEMBLrel. 04, Created)
DT 01-NOV-1996 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE GIN11 protein (Fragment).
GN GIN11 OR YLL065W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Wedler H., Wedler E., Scharfe M., Wambutt R.
RC Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
PP SEQUENCE FROM N.A.
RA MIPS;
PI Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: Z73189; CAA97518.2; -
DR SDB: S0003988; GIN11.
FT NON_TER 1 1
SQ SEQUENCE 9 AA: 1019 MW: 4F21A9C449D8B73P CF 64:

Query Match 28.6%; Score 2; DB 3; length 8;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FT 6
DB 6 FT 7

RESULT 13
Q9H4D3 PRELIMINARY: PRT: 8 AA.
ID Q9H4D3;
AC Q9H4D3;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE LIM domain only 1 protein (Fragment).
GN LM01.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BL00D;
RA Rueckmann T., Winterpacht A., Hankele T., Schmidt F.W., Fabel B.
RT "Human PAC clone hCIP704K03781 (pM1781K3), sequenced in DHS probes.
(Comparative sequencing of a 1 Mb Region in Man (Chromosome 11p15) and
Mouse (Chromosome 7))."
RL Submitted (Apr-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ276661; CAC14573.1; -
FT NON_TER 8 8
SQ SEQUENCE 8 AA: 599 MW: F4A133AA721596 CF 64:

Query Match 28.6%; Score 2; DB 4; length 8;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KE 3
DB 6 KE 7

RESULT 14
ID Q15888 PRELIMINARY: PRT: 8 AA.
AC Q15888;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

```

DI 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE (clone XP1588A) (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PLACENTA;
 RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
 RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,
 RA Caskey C.T.H.;

RT "Isolation of chromosome-specific genes by reciprocal probing of
 RT arrayed cDNAs and cosmid libraries."
 RL Hum. Mol. Genet. 0:0-0(1995).

DR EMRL; L32069; AAA73878.1; -;
 FT NON_TER 1 1
 FT NON_TER 8 8

SQ SEQUENCE 8 AA: 1068 MW: 0315A37EAB5E0763 CR04;
 Query Match 28.6%; Score 2; DB 4; Length 8;
 Best Local Similarity 100.0%; Pred. No. 6.7e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 EY 4

DB 4 EY 4

RESULT 15

Q15893 ID Q15893 PRELIMINARY; PRT; 8 AA.
 AC Q15893;
 DI 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE (clone XP587A) (Fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.

RC TISSUE=PLACENTA;
 RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
 RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,
 RA Caskey C.T.H.;

RT "Isolation of chromosome-specific genes by reciprocal probing of
 RT arrayed cDNAs and cosmid libraries."
 RL Hum. Mol. Genet. 0:0-0(1995).

DR EMRL; L32073; AAA3883.1; -;
 FT NON_TER 1 1
 FT NON_TER 8 8

SQ SEQUENCE 8 AA: 874 MW: DAA1B6D7376456C5 CR04;

Query Match 28.6%; Score 2; DB 4; Length 8;
 Best Local Similarity 100.0%; Pred. No. 6.7e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 TS 7

DB 7 TS 8

Search Completed: April 29, 2003, 08:53.23
 Job time : 29.4167 secs

FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 8 8 AMIDATION.
 SU SEQUENCE 8 AA: 949 MW: 86786771A9D1A736 CRC64;
 Query Match 28.6%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.1e-05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0;
 QY 5 FT 6
 DB 4 FT 5

RESULT 10
 HTF2_PERAM STANDARD: PRI: 8 AA.
 AC P04549;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE Hyperichthaloasmin factor II (Neuropeptide M II) (Periplaneta CC 2)
 DE (PeA-CAH-II) (LeD-CC-II) (Hyperichthaloasmin neuropeptide II).
 DE Periplaneta americana (American cockroach).
 OS Leptinotarsa decemlineata (Colorado potato beetle) and
 OS Blatta orientalis (Oriental cockroach).
 CC Eukaryota; Metazoa; Arthropoda; Mandibulata; Insecta; Hexapoda;
 CC Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
 CC Blattodea; Blattellidae; Periplaneta.
 CC NCBI_TaxID=578; 7539; 6976;
 RN [1]
 RP SEQUENCE.
 RC SPECIES-P.americana;
 RX METLINE=804659; PubMed=5548628;
 RA Witten J.L., Schaffer M.H., O'Shea M., Dock J., Hemling M.E.,
 RA Riechart K.L., Jr.
 RT "Structures of two cockroach neuropeptides synthesized by fast atom
 RT bombardment mass spectrometry."
 RL Biochem. Biophys. Res. Commun. 124:350-356(1984).
 RN [2]
 RP SEQUENCE.
 RC SPECIES-P.americana;
 RX MEDLINE=84298179; PubMed=2571255;
 RA Scarborough R.M., Jamieson G.C., Kalish P., Warner S.J., McEnroe G.A.,
 RA Miller C.A., Schooley D.A.
 RT "Isolation and primary structure of two peptides with
 RT cardioacceleratory and hyperglycemic activity from the corpora
 RT cardiaca of Periplaneta americana."
 RL Proc. Natl. Acad. Sci. U.S.A. 81:5575-5579(1984).
 RN [3]
 RP SEQUENCE.
 RC SPECIES-B.orientalis; TISSUE=Corpora cardiaca;
 RX MEDLINE=90253650; PubMed=2340112;
 RA Gaede G., Pinehart K.L., Jr.
 RT "Primary structures of hyperichthaloasmin neuropeptides isolated from
 RT the corpora cardiaca of the cockroaches Leucophaea maderae, and
 RT Chromaphorina porteri. Blattea germanica and Blatta orientalis
 RT and of the stick insect Extatosoma tiaratum assigned by tandem fast
 RT atom bombardment mass spectrometry."
 RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).
 CC -1- FUNCTION: HYPERICHTHALOASMIN FACTORS ARE NEUROPEPTIDES THAT
 CC ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
 CC THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
 CC -1- SIMILARITY: BELONGS TO THE AKH / RHTH / APCH FAMILY.
 UR PIP: A05170; A05170;
 DR PIP: S08496; S08496;

DR PIR: B44960; B44960.
 DR PIR: B49823; B49823.
 DR InterPro: IPR002047; AKH.
 DR PROSITE: PS00256; AKH; 1.
 KW Neuropeptide: Amidation.
 FT MOD_RES 1 1
 FT MOD_RES 8 8 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 8 8 AMIDATION.
 SU SEQUENCE 8 AA: 1006 MW: 86745771A9D1A736 CRC64;
 Query Match 28.6%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.1e-05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0;
 QY 5 FT 6
 DB 4 FT 5

RESULT 11
 LMT2_LOCM1 STANDARD: PRI: 8 AA.
 AC P22396;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 01-AUG-1991 (Rel. 19, Last annotation update)
 DE Locustanoylrokin 2 (LOM-MI-2).
 OS Locusta migratoria (Migratory locust).
 CC Eukaryota; Metazoa; Arthropoda; Mandibulata; Insecta; Hexapoda;
 CC Insecta; Pterygota; Neoptera; Orthopteroidea; Orthoptera; Acridoidea;
 CC Acridomorpha; Acridoidea; Acrididae; Caelipodinae; Locusta.
 CC NCBI_TaxID=7004;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Corpora cardiaca;
 RA Schoofs L., Holman G.M., Hayes T.K., Natchman P.J., de Loof A.,
 RT "Isolation, identification and synthesis of locustanoylrokin II, an
 RT additional neuropeptide of Locusta migratoria. Member of the
 RT cephalomyotropic peptide family."
 RL Insect Biochem. 20:479-484(1990).
 RN [2]
 RP FUNCTION: MEDIATES VISCEAL MUSCLE CONTRACTILE ACTIVITY.
 CC -1- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
 DE InterPro: IPR001484; PYROKININ.
 DE PROSITE: PS00539; PYROKININ; 1.
 KW Neuropeptide: Amidation; Pyrokinin.
 FT MOD_RES 8 8
 FT MOD_RES 8 8 AMIDATION.
 SU SEQUENCE 8 AA: 934 MW: 26341771A9CAA87B CRC64;
 Query Match 28.6%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.1e-05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0;
 QY 5 FT 6
 DB 4 FT 5

RESULT 12
 LPK_LEUMA STANDARD: PRI: 8 AA.
 AC P13049;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE Leukopyrokinin (LPK) (LEM-PK).
 OS Leucophaea maderae (Madeira cockroach).
 CC Eukaryota; Metazoa; Arthropoda; Mandibulata; Panciustacea; Hexapoda;
 CC Insecta; Pterygota; Neoptera; Orthopteroidea; Blattaria;
 CC Blattodea; Blaberidae; Leucophaea.
 CC NCBI_TaxID=6498;
 RN [1]
 RP SEQUENCE.
 RX METLINE=8626904; PubMed=3015140;

RA Nachman R.J., Holman G.M., Cook B.J.:
 RT "Active fragments and analogs of the insect neuropeptide
 RT leucopyrokinin: structure-function studies."
 RL Biochem. Biophys. Res. Commun. 137:936-942(1986).
 BN (2).
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE-Head;
 RA MEDLINE=8705251; PubMed=2877794;
 RX Holman G.M., Cook B.J., Nachman R.J.:
 RT "Primary structure and synthesis of a bioactive peptide
 RT neuropeptide isolated from the cockroach, *Nauphoeta cinerea*."
 RL Comp. Biochem. Physiol. 85C:219-224(1986).
 CC -1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTION LE ACTIVITY
 CC (MYOTROPIC ACTIVITY).
 CC -1- MISCELLANEOUS: AN ANALOG WITHOUT THE N-TERMINAL PCA RESIDUE WAS
 CC SYNTHESIZED AND FOUND TO EXHIBIT GREATER ACTIVITY (144%) THAN THE
 CC PARENT NEUROPEPTIDE. THE PORTION OF THE SEQUENCE OF LEK MOST
 CC CRITICAL FOR THE MYOTROPIC PROPERTIES IS LIMITED TO THE
 CC PENTAPEPTIDE FRAGMENT FTPLR.
 CC -1- SIMILARITY: BELONGS TO THE PYROKININ FAMILY
 CC PIR: A23967; A23957.
 DE InterPro: IPR001494; Pyrokinin.
 CH PROSITE: PS00549; PYROKININ: 1.
 KW Neuropeptide; Amidation; Pyrokinin
 FT MOD_RES 1 1 PYROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA: 949 MW: 92411771A95A1B6 GRN4;
 Query Match 29.6%, Score 2, DB 1, Length 8,
 Best Local Similarity 100.0%, Pred. No. 1 la-05;
 Matches 2, Conservative 0, Mismatches 0, Indels 0, Gaps 0;
 QY 6 TS 7
 DB 2 TS 3

RESULT 13
 ID ORMY_ORC11 STANDARD: PRT: 8 AA
 AC P82455;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Oremyotroptin (ORM)
 CC Oremyotroptin (ORM) (Spinychek crayfish).
 CC Eukaryota, Metazoa, Arthropoda, Mandibulata, Pancrustacea, Crustacea,
 CC Malacostraca, Eumalacostraca, Eucarida, Decapoda, Pseudosquilla,
 CC Astacidea, Astacidae, Cambaridae, Orconectidae.
 CC NCBI_TaxID=28179;
 RN (1)
 RP SEQUENCE, MASS SPECTROMETRY, AND AMIDATION.
 RC TISSUE-Hindgut.
 RX MEDLINE=20411310; PubMed=10952880;
 RA Birken H., Burdick S., Saurer A., Keller R.J.
 RT "Two prokinins and the novel octapeptide ormyotroptin in the hindgut
 RT of the crayfish *Oreoreetes limosus* identified by immunohistochemistry
 RT neuropeptides originating together in neurons of the terminal
 RT abdominal ganglion."
 RL J. Exp. Biol. 203:2807-2818(2000).
 CC -1- FUNCTION: MYOTROPIC PEPTIDE, ENHANCES BOTH THE FREQUENCY AND
 CC AMPLITUDE OF SPONTANEOUS HINDGUT CONTRACTIONS. IT IS SYNTHESIZED
 CC BY ABDOMINAL GANGLIONIC NEURONS.
 CC -1- MASS SPECTROMETRY: MW=904.8; METHOD=FAB.
 KW Amidation; Neuropeptide.
 FT MOD_RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA: 505 MW: 57086161A9C1A4 GRN4;
 Query Match 29.6%, Score 2, DB 1, Length 8;
 Best Local Similarity 100.0%, Pred. No. 1 la-05;
 Matches 2, Conservative 0, Mismatches 0, Indels 0, Gaps 0;
 QY 5 FT 6

DB 4 FT 5

RESULT 14
 ID CCAP_CARMA STANDARD: PRT: 9 AA.
 AC P38556;
 DT 01-OCT-1994 (Rel. 40, Created)
 DT 01-OCT-1994 (Rel. 40, Last sequence update)
 DT 15-JUN-1996 (Rel. 37, Last annotation update)
 DE Cardioactive peptide (CCAP).
 CC Cardioactive peptide (CCAP).
 CC Cardinus maenas (Common shore crab) (Green crab).
 CC Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
 CC Tenebrio molitor (Yellow mealworm) and
 CC Spodoptera eridania (Southern armyworm).
 CC Eukaryota, Metazoa, Arthropoda, Mandibulata, Pancrustacea, Crustacea,
 CC Malacostraca, Eumalacostraca, Eucarida, Decapoda, Eumecystacea,
 CC Brachyura, Eubrachyura, Portunoidae, Portunidae, Carcinus.
 CC NCBI_TaxID=6759, 7130, 7067, 37547;
 RN (1)
 RP SEQUENCE.
 RC SPECIES=Carcinus; TISSUE=pericardial organs;
 RA Staudier J., Hilbich C., Beyreuther K., Keller R.J.
 RT "Unusual cardioactive peptide (CCAP) from pericardial organs of the
 RT shore crab *Cardinus maenas*."
 RL Proc. Natl. Acad. Sci. U.S.A. 84:575-579(1987).
 RN (2)
 RP SEQUENCE.
 RC SPECIES=M. sexta;
 RX MEDLINE=3055143; PubMed=1125284;
 RA Cheung C.C., Loi P.K., Sylwester A.W., Lee T.D., Tublitz N.J.:
 RT "Primary structure of a cardioactive neuropeptide from the tobacco
 RT hawkmoth, *Manduca sexta*."
 RL FEBS Lett. 313:165-168(1992).
 RN (3)
 RP SEQUENCE.
 RC SPECIES=T. molitor, and S. eridania; TISSUE=Head;
 RX MEDLINE=94176032; PubMed=8129851;
 RA Furuya K., Iino S., Reynolds S.F., Ota R.B., Hackett M.,
 RA Schooley D.A.:
 RT "Isolation and identification of a cardioactive peptide from *Tenebrio*
 RT molitor and *Spodoptera eridania*."
 RL Biol. Chem. Hoppe-Seyler 274:1065-1074(1993).
 CC -1- FUNCTION: THE EFFECT OF CCAP IS BOTH INO- AND CHRONOTROPIC.
 CC -1- TISSUE SPECIFICITY: STORED IN PERICARDIAL ORGANS AND RELEASED
 CC INTO THE HEMOLYPH.
 CC PIR: A23929, A23964,
 CC PIR: 227223, 527233,
 CC PIR: 227223, 527233,
 KW Neuropeptide; Amidation.
 FT MOD_RES 3 9
 FT DISULFID 3 9
 FT MOD_RES 9 9
 SQ SEQUENCE 9 AA: 474 MW: 55861A9C0C44 GRN4;
 Query Match 29.6%, Score 2, DB 1, Length 9;
 Best Local Similarity 100.0%, Pred. No. 1 la-05;
 Matches 2, Conservative 0, Mismatches 0, Indels 0, Gaps 0;
 QY 5 FT 6
 DB 6 FT 7

RESULT 15
 ID COXE_THUCR STANDARD: PRT: 9 AA.
 AC P80975;
 DT 01-NOV-1997 (Rel. 45, Created)
 DT 01-NOV-1997 (Rel. 45, Last sequence update)
 DT 15-JUN-1996 (Rel. 37, Last annotation update)
 DE Cytochrome c oxidase polypeptide Via (COX I 9.3.1) (Fragment).
 CC *Thunnus obesus* (Blueeye tuna).
 CC Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;

CC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 CC Acanthomorpha; Acanthopterygii; Percormorpha; Perciformes; Scombroidei;
 CC Scombridae; Thunnus.
 OX NCBI_TaxID=8241;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Heart;
 FX MEDLINE=97454241, PubMed=9310366;
 RA Arnold S., Lee I., Kim M., Song E., Linder D., Gottspeich F.,
 RA Kadenbach B.;
 RT "The subunit structure of cytochrome-c oxidase from tuna heart and
 RT liver";
 RL Eur. J. Biochem. 248:99-103(1997).
 CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
 CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
 CC MITOCHONDRIAL ELECTRON TRANSPORT.
 CC -!- CATALYTIC ACTIVITY: 4 ferri-cytochrome c (2) + 4 ferri-cytochrome
 CC c + 2 H(2)O.
 CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
 CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIA FAMILY.
 DE InterPro: IPR001449; COX6A.
 DE PROSITE: PS01329; COX6A; PARTIAL.
 KW Oxidoreductase; Inner membrane; Mitochondrion.
 FT NON_TER 1 1
 FT NON_TER 9 9
 SQ SEQUENCE 9 AA: 1136 MW: 626072929077658 (Uncl64);

Query Match 28.6%; Score 2; DB 1; length 9;
 Best Local Similarity 100.0%; Pred.No. 1.1e+04.
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KE 3
 Db 1 KE 2

Search completed: April 29, 2003, 08:52:29
 Job time : 17.3333 secs


```

RESULT 4
B37325
pap fimbrial regulatory protein papi - Escherichia coli (fragment)
C:Species: Escherichia coli
C:Date: 11-Sep-1992 #sequence_revision 11-Sep-1992 #text_change 23-Mar-1993
C:Accession: B37325
R:Baarsen, B.A.; Blyvo, L.B.; Skinner, B.S.; Low, P.A.
J. Bacteriol. 173, 1789-1800, 1991
A:Title: Evidence for a methylation-blocking factor (mbf) locus involved in pap pilus ex
A:Reference number: A37325; MUID:91154136; PMID:171957
A:Accession: B37325
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-5 <BRA>
A:Cross-references: GB:M63747

Query Match 28.6% Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2 Re+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YF 4
DB 3 YF 4

RESULT 4
PT0278
14 heavy chain C2D3 region (clone 4-68) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0278
R:Vanada, M.; Wasserman, P.; Feilichard, B.A.; Shaw, S.; Catton, A.J.; Faveria, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
A:Reference number: PT0222; MUID:91108337; PMID:1694102
A:Accession: PT0278
A:Molecule type: DNA
A:Residues: 1-5 <YAM>
A:Experimental source: B lymphocyte
C:Keywords: heterotetramer; immunoglobulin

Query Match 28.6% Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2 Re+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YF 5
DB 1 YF 2

RESULT 5
PT0644
T-cell receptor beta chain V-D-1 region (111-12) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 10 May 1997
C:Accession: PT0644
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0644
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-5 <FEE>
A:Experimental source: newborn thymus, strain BALB.
C:Keywords: T-cell receptor

Query Match 28.6% Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2 Re+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 YF 6
DB 1 YF 6

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DB 4 YF 5

RESULT 6
H44817
34.5K structural protein - Leuconostoc oenos phase P32 (fragment)
C:Species: Leuconostoc oenos phase P32
C:Date: 31-Mar-1993 #sequence_revision 22-May-1998 #text_change 22-May-1998
C:Accession: H44817
P:Arendt, E.K.; Lonvaud, A.; Hammes, W.P.
J. Gen. Microbiol. 137, 2135-2139, 1991
A:Title: Lysogeny in Leuconostoc oenos.
A:Reference number: A44817; MUID:92085033; PMID:1748868
A:Accession: H44817
A:Molecule type: protein
A:Residues: 1-5 <ARE>
A:Note: sequence extracted from NCRP backbone (NCRP:70332)

Query Match 28.6% Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2 Re+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TS 7
DB 3 TS 4

RESULT 7
F44817
34.5K structural protein - Leuconostoc oenos phase P54 (fragment)
C:Species: Leuconostoc oenos phase P54
C:Date: 31-Mar-1993 #sequence_revision 22-May-1998 #text_change 22-May-1998
C:Accession: F44817
P:Arendt, E.K.; Lonvaud, A.; Hammes, W.P.
J. Gen. Microbiol. 137, 2135-2139, 1991
A:Title: Lysogeny in Leuconostoc oenos.
A:Reference number: A44817; MUID:92085033; PMID:1748868
A:Accession: F44817
A:Molecule type: protein
A:Residues: 1-5 <ARE>
A:Note: sequence extracted from NCRP backbone (NCRP:70335)

Query Match 28.6% Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2 Re+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TS 7
DB 3 TS 4

RESULT 8
B44817
34.5K structural protein - Leuconostoc oenos phase P211-15 (fragment)
C:Species: Leuconostoc oenos phase P211-15
C:Date: 31-Mar-1993 #sequence_revision 22-May-1998 #text_change 22-May-1998
C:Accession: B44817
P:Arendt, E.K.; Lonvaud, A.; Hammes, W.P.
J. Gen. Microbiol. 137, 2135-2139, 1991
A:Title: Lysogeny in Leuconostoc oenos.
A:Reference number: A44817; MUID:92085033; PMID:1748868
A:Accession: B44817
A:Molecule type: protein
A:Residues: 1-5 <ARE>
A:Note: sequence extracted from NCRP backbone (NCRP:70342)

Query Match 28.6% Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2 Re+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TS 7
DB 3 TS 4

```

```

Dt      4 TS 4

RESULT 4
D44817
35K structural protein - Leuconostoc oenos phage PA5-12 (fragment)
C:Species: Leuconostoc oenos phage PA5-12
C:Date: 31-Mar-1993 #sequence_revision 22-Mar-1993 #text_change 22-May-1993
C:Accession: D44817
R:Arendt, E.F.; Leonard, A.; Hammes, W.P.
J Gen Microbiol. 137, 2125-2139, 1991
A:Title: Lysogeny in Leuconostoc oenos.
A:Reference number: A44817, MUID:9298323, PMID:1741968
A:Accession: D44817
A:Molecule type: protein
A:Residues: 1-5 <ARE>
A>Note: sequence extracted from NCBI backbone (NCBI:70340)

Query Match      28.6%, Score 2, DB 2, Length 5,
Best Local Similarity 100.0%, Pred. No. 2.8e+05;
Matches 2, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

QY 6 TS 7
DB 4 TS 4

RESULT 10
S02617
alcohol dehydrogenase (EC 1.1.1.1) chi - horse (fragment)
C:Species: Equus caballus (domestic horse)
C:Date: 28-Feb-1990 #sequence_revision 29-Feb-1992 #text_change 31-Dec-1997
C:Accession: S02617
R:Fairwell, T.; Tolia, P.; Kaiser, P.; Holmquist, P.; Pares, X.; Vallee, B.L.; Jourdain
PERS Lett. 222, 99-103, 1987
A:Title: Acetylated N-terminal structures of class III alcohol dehydrogenases. Differences
A:Reference number: S02617; MUID:88005160; PMID:3676405
A:Accession: S02617
A:Molecule type: protein
A:Residues: 1-6 <FAI>
C:Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology
C:Keywords: alcohol metabolism; NAD, oxidoreductase.

Query Match      28.6%, Score 2, DB 2, Length 6;
Best Local Similarity 100.0%, Pred. No. 2.8e+05;
Matches 2, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

QY 1 IK 2
DB 5 IK 6

RESULT 11
A31263
dihydrofolate reductase, EC 1.5.1.3, / thymidylate synthase (EC 2.1.1.45) - Plasmodium f
C:Species: Plasmodium falciparum
C:Date: 29-Feb-1990 #sequence_revision 29-Feb-1990 #text_change 20-Mar-1997
C:Accession: A31263
R:Peterson, D.S.; Walliker, D.; Wellens, T.E.
Proc. Natl. Acad. Sci. U.S.A. 85, 9114-9118, 1988
A:Title: Evidence that a point mutation in dhfrdrl late reduction thymidylate synthase
A:Reference number: A31263; MUID:89057885; PMID:3090419
A:Accession: A31263
A>Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-6 <PET>
C:Keywords: methylenetetrahydrofolate; NADP; oxidoreductase.

Query Match      28.6%, Score 2, DB 2, Length 6;
Best Local Similarity 100.0%, Pred. No. 2.8e+05;
Matches 2, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

QY 6 TS 7

Dt      4 TS 4

Db      1 TS 2

RESULT 12
S17976
glucose isomerase - Thermoplasma acidophilum saccarolyticum (fragment)
C:Species: Thermoplasma acidophilum saccarolyticum
C:Date: 12-Feb-1998 #sequence_revision 12-Feb-1998 #text_change 17-Apr-1998
C:Accession: S17976
R:Lee, C.; Zeikus, J.G.
Biochem. J. 273, 565-571, 1991
A:Title: Purification and characterization of the most stable glucose isomerase from clo
A:Reference number: S15119; MUID:91144536; PMID:1996956
A:Accession: S17976
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-7 <LEE>
A>Note: the sequence from page 568 is inconsistent with that from page 566 in having
A>Note: the source is designated as Thermoplasma acidophilum strain PEA

Query Match      28.6%, Score 2, DB 2, Length 7;
Best Local Similarity 100.0%, Pred. No. 2.8e+05;
Matches 2, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

QY 4 YF 5
DB 4 YF 5

RESULT 13
F00254
18K protein 5507 - rice (strain Nihonbare) (fragment)
C:Species: Oryza sativa (rice)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Mar-1995
C:Accession: F00254
R:Tsugita, A.
submitted to JIPID, April 1993
A:Reference number: F00206
A:Accession: F00254
A:Molecule type: protein
A:Residues: 1-7 <TSO>
A:Experimental source: leaf, chloroplast, strain Nihonbare
A>Note: molecular weight 18K, pI 4.4

Query Match      28.6%, Score 2, DB 2, Length 7;
Best Local Similarity 100.0%, Pred. No. 2.8e+05;
Matches 2, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

QY 2 KE 3
DB 5 KE 6

RESULT 14
S33244
neuro-modulatory peptide Wamide1, from African snail
C:Species: Achatina fulica (Giant African snail)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
C:Accession: S33244
R:Minikata, H.; Ishii, T.; Muraoka, Y.; Fukuyasu, M.; Nishida, F.
FEBS Lett. 323, 104-108, 1993
A:Title: Wamide1, 2 and 3: novel neuromodulatory peptides isolated from snail
A:Reference number: S33244; MUID:93265912; PMID:8495720
A:Accession: S33244
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-7 <MIN>

Query Match      28.6%, Score 2, DB 2, Length 7;
Best Local Similarity 100.0%, Pred. No. 2.8e+05;
Matches 2, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

```

QY 2 KE 3
 II
 Db 2 KE 3

RESULT 15

PC1316
 large granule L3 chain - horseshoe crab (Tachyporus tridentatus) (fragment)
 C:Species: Tachyporus tridentatus
 C:Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 07-May-1999
 C:Accession: PC1316
 R:Shigenaga, T.; Takayama, Y.; Kawasaki, S.; Seki, N.; Muta, T.; Ichi, Y.; Ito, A.; Iwa
 J. Biochem. 114, 307-316, 1993
 A:Title: Separation of large and small granules from horseshoe crab (Tachyporus tridentatus)
 A:Reference number: PC1309; MUIP-94110249; PMID-8284718
 A:Accession: PC1316
 A:Molecule type: protein
 A:Residues: 1-7 <SH1>
 C:Comment: This protein participates in immobilization of invading microbes.

Query Match 28.6%; Score 2; DB 2; length 7;
 Best Local Similarity 100.0%; Pred. No. 2.8e+01;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TS 7
 II
 Db 1 TS 2

Search completed: April 29, 2003, 08:54:19
 Job time : 30.1667 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 25, 2003, 09:30:19, Search size 58, 9167 sequences
(without alignments)
15,842 Million cell updates/sec

Title: US-09-647-749A-2

Perfect score: 7

Sequence: 1 IKEYETS 7

Scoring table: colgo
Gapop 60.0, Gapext 60.0

Searched: 908476 seqs, 13425620 residues

Word size: 0
Total number of hits satisfying chosen parameters: 174064

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: Listing first 45 summaries

Database: A_Geneseq_101002:*

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2. /SID2/qcdata/geneseq/geneseq-emb1/AA1967.DAT:
3. /SID2/qcdata/geneseq/geneseq-emb1/AA1968.DAT:
4. /SID2/qcdata/geneseq/geneseq-emb1/AA1969.DAT:
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9. /SID2/qcdata/geneseq/geneseq-emb1/AA1974.DAT:
10. /SID2/qcdata/geneseq/geneseq-emb1/AA1975.DAT:
11. /SID2/qcdata/geneseq/geneseq-emb1/AA1976.DAT:
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23. /SID2/qcdata/geneseq/geneseq-emb1/AA1988.DAT:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7	100.0	7	AA1966	Hiv-1 gp120 indyco
2	4	57.1	5	AA1967	P02 motif sequence
3	4	57.1	5	AA1968	Glycophorin C C-te
4	4	57.1	5	AA1969	Glycophorin C C-te
5	4	57.1	6	AA1970	P02 motif sequence
6	4	57.1	6	AA1971	Glycophorin C C-te
7	4	57.1	6	AA1972	Glycophorin C C-te
8	4	57.1	6	AA1973	P02 motif sequence
9	4	57.1	7	AA1974	Glycophorin C C-te
10	4	57.1	7	AA1975	Glycophorin C C-te

11	4	57.1	8	22	AA1966	P02 motif sequence
12	4	57.1	8	22	AA1967	Glycophorin C C-te
13	4	57.1	8	22	AA1968	Glycophorin C C-te
14	4	57.1	8	16	AA1969	Peptide fragment (
15	4	57.1	9	17	AA1970	Antigenic peptide,
16	4	57.1	9	20	AA1971	P53 epitope (aa 12
17	4	57.1	9	20	AA1972	Amino acid sequence
18	4	57.1	9	20	AA1973	HLA-A2 binding p53
19	4	57.1	9	21	AA1974	Proteoglycan cell
20	4	57.1	9	21	AA1975	P53 DR 3a motif bi
21	4	57.1	9	22	AA1976	IF CSP immunogenic
22	4	57.1	9	23	AA1977	159P1P related HL
23	4	57.1	9	23	AA1978	159P1P related HL
24	4	57.1	10	17	AA1979	159P1P related immu
25	4	57.1	10	21	AA1980	Proteoglycan cell
26	4	57.1	10	22	AA1981	Humanized anti-tis
27	4	57.1	10	22	AA1982	Human complementar
28	4	57.1	10	23	AA1983	159P1P related HL
29	4	57.1	10	23	AA1984	159P1P related HL
30	4	57.1	10	23	AA1985	159P1P related HL
31	4	57.1	10	23	AA1986	159P1P related HL
32	4	57.1	10	23	AA1987	159P1P related HL
33	4	57.1	10	23	AA1988	159P1P related HL
34	4	57.1	10	23	AA1989	159P1P related HL
35	3	42.9	4	21	AA1990	MHC class II prote
36	3	42.9	4	21	AA1991	Copeptide useful :
37	3	42.9	4	22	AA1992	Membrane surface
38	3	42.9	4	22	AA1993	P53 motif sequenc
39	3	42.9	4	22	AA1994	C146 C-terminal co
40	3	42.9	4	22	AA1995	Glycophorin C C-te
41	3	42.9	4	22	AA1996	C146 C-terminal co
42	3	42.9	4	22	AA1997	Glycophorin C C-te
43	3	42.9	4	23	AA1998	BYF N terminal pr
44	3	42.9	4	23	AA1999	Cell death protect
45	3	42.9	5	11	AA1990	D element in estro

ALTERNATES

```
RESULT 1
AA1966
1. AA1966 standard peptide, 7 AA.
XX
AC AA1966
XX
XX 15 20 200 first entry
XX
XX HIV-1 HIV-1 related head and tail leath inhibiting peptide #2
XX
XX gp120 (91-94) E protein disease, HIV-1 envelope protein gp120
XX
XX Leishmania, a sessile flagellated chemotaxis viral infection
XX
XX Neutralizing activity of glycoprotein, neurotoxicity, memory loss
XX
XX Neutralizing activity of glycoprotein, neurotoxicity, memory loss
XX
XX dementia; depression, psychosis, opportunistic infection
XX
XX neurotoxicity; inflammatory neurological disease; multiple sclerosis
XX
XX tropical spastic paraparesis; Alzheimer's disease.
XX
XX Synthetic.
XX
XX WO9951254-A1.
XX
XX 14-OCT-1999.
XX
XX 06-APP-1999: 0600-0907514.
XX
XX 06-APP-1999: 0600-090836.
XX
XX (ADIN-) ADVANCED IMMUNIT INC.
XX
XX Part C, Buff M;
XX
XX WPI: 1000-623645/54.
XX
```

PT New peptides useful for inhibiting human immunodeficiency virus type 1
 PT (HIV-1) gp120 induced neuronal cell death
 XX
 PS Claim 1: Page 11: 16pp; English.
 XX
 CC AAY49695 and AAY49696 represent peptides which inhibit HIV 1 gp120
 CC induced neuronal cell death. Pharmaceutical compositions containing the
 CC peptides are useful for treating symptoms caused by neuronal cell loss.
 CC such conditions especially associated with HIV infection include
 CC encephalopathies, neuropathies, memory loss, dementia, depression,
 CC psychosis and opportunistic infections. The peptides act as antagonists
 CC of gp120-mediated neurotoxicity and subsequent neuronal degeneration.
 CC This enables therapeutic treatment of HIV infection and other
 CC inflammatory neurological diseases, including multiple sclerosis,
 CC tropical spastic paraparesis and Alzheimer's disease.
 XX
 SQ Sequence 7 AA:
 Query Match 100.0%; Score 7; DB 20; Length 7;
 Best Local Similarity 100.0%; Pred No. 7.4e-5;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KEYFITS 7
 I I I I I I I
 Db 1 KEYFITS 7
 RESULT 2
 AAB55781
 ID AAB55781 standard; Peptide: 5 AA.
 XX
 AC AAB55781:
 XX
 DT 07-MAR-2001 (first entry)
 XX
 DE PDZ motif sequence #12.
 DE Hematopoietic cell PDZ PL autoimmune disease, inflammation,
 KW allergy; asthma; multiple sclerosis; cancer infection.
 KW Synthetic.
 OS
 XX Homo sapiens.
 XX W0200069896-A2.
 XX
 XX 23-NOV-2000.
 XX
 XX 12-MAY-2000; 2000WS-US13161.
 XX
 XX 14-MAY-1999; 990S-0134114.
 XX 14-MAY-1999; 990S-0134117.
 XX 14-MAY-1999; 990S-0134118.
 XX 21-OCT-1999; 990S-0160460.
 XX 26-OCT-1999; 990S-0162498.
 XX 13-DEC-1999; 990S-0170453.
 XX 14-JAN-2000; 2000US-0171194.
 XX 14-FEB-2000; 2000US-0182796.
 XX 11-APR-2000; 2000US-0196460.
 XX 11-APR-2000; 2000US-0196527.
 XX
 XX (ARBO-) ARBOR VITA CORP.
 XX
 XX Lu PS:
 XX
 XX WPI: 2001-080245/09.
 XX
 PT Modulating a biological function of an endothelial cell or
 PT hematopoietic cell, useful for treating autoimmune diseases and
 PT infectious diseases, by administering an antagonist that inhibits
 PT binding between a PDZ protein and a PL protein.
 XX
 XX Disclosure: Page 87-94; 141pp; English.
 XX
 XX The present invention relates to a new method for modulating a

CC biological function of an endothelial cell or hematopoietic cell. The
 CC method involves introducing into a cell, an antagonist that inhibits
 CC binding between a PDZ protein and a PL protein. The inhibitor is used
 CC to treat a disease mediated by hematopoietic cells, e.g. autoimmune
 CC disease. It may also be used to prevent transplantation rejection of
 CC a solid organ transplant. The method may also be used in the treatment
 CC of inflammation, allergy, inflammatory bowel diseases, ulcerative
 CC colitis, ileitis, psoriasis, asthma, atopic dermatitis, autoimmune
 CC diseases (e.g. rheumatoid arthritis, multiple sclerosis,
 CC insulin-dependent diabetes, Hashimoto thyroiditis, osteoarthritis,
 CC graft rejection, transplantation rejection), atherosclerosis, cancer,
 CC infectious diseases, ischemia, vasculitis and Crohn's disease.
 XX
 SQ Sequence 5 AA:
 Query Match 57.1%; Score 4; DB 22; Length 5;
 Best Local Similarity 100.0%; Pred. No. 7.8e-05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 KEYF 5
 I I I I I
 Db 1 KEYF 4
 RESULT 3
 AAB57613
 ID AAB57613 standard; Peptide: 5 AA.
 XX
 AC AAB57613:
 XX
 DT 12-MAR-2001 (first entry)
 XX
 DE Glycophorin C C-terminal core sequence #2.
 XX
 KW Endothelial cell; hematopoietic cell; PDZ domain protein;
 KW PL domain protein; leukocyte activation; T cell surface receptor;
 KW synapse formation; transmembrane neurotransmitter receptor;
 KW autoimmune disease; transplantation rejection; inflammation; allergy;
 KW inflammatory bowel disease; ulcerative colitis; ileitis; psoriasis;
 KW asthma; atopic dermatitis; atherosclerosis; cancer; infectious disease;
 KW ischemia; vasculitis; Crohn's disease.
 XX
 OS Homo sapiens.
 XX W0200069897 A2.
 XX
 XX 23-NOV-2000.
 XX
 XX 12-MAY-2000; 2000WS-US13166.
 XX
 XX 14-MAY-1999; 990S-0134114.
 XX 14-MAY-1999; 990S-0134117.
 XX 14-MAY-1999; 990S-0134118.
 XX 21-OCT-1999; 990S-0160460.
 XX 26-OCT-1999; 990S-0162498.
 XX 13-DEC-1999; 990S-0170453.
 XX 14-JAN-2000; 2000US-0176195.
 XX 14-FEB-2000; 2000US-0182796.
 XX 11-APR-2000; 2000US-0196460.
 XX 11-APR-2000; 2000US-0196527.
 XX
 XX (ARBO-) ARBOR VITA CORP.
 XX
 XX Lu PS:
 XX
 XX WPI: 2001-025003/03.
 XX
 PT New inhibitors of binding of a PDZ protein and PL protein for
 PT inhibiting T cell-mediated response by hematopoietic cells, or for
 PT treating diseases characterized by inflammatory and humoral immune
 PT responses; e.g. inflammation; cancer.
 XX
 XX Disclosure: Page 93, 139pp, English.


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XX PR 14-MAY-1999; 990S-0134114.
XX PR 14-MAY-1999; 990S-0134117.
XX PR 14-MAY-1999; 990S-0134118.
XX PR 21-OCT-1999; 990S-0160860.
XX PR 29-OCT-1999; 990S-0162498.
XX PR 13-DEC-1999; 990S-0170453.
XX PR 14-JAN-2000; 20000S-0176195.
XX PR 14-FEB-2000; 20000S-0182296.
XX PR 11-APR-2000; 20000S-0196460.
XX PR 11-APR-2000; 20000S-0196527.
XX PA (ARBO-) APPROX VITA CORP.
XX PI Lu PS.
XX DR WPI: 2001-061214/07.
XX PT Modulating a biological function of a hematopoietic cell for treating
XX PT an allergic response, or diseases mediated by immune system cells,
XX PT comprises introducing into the cell a PDZ domain protein that inhibits
XX PT an inhibitor.
XX PS Disclosure: Page 96; 143pp; English.
XX CC The present invention relates to a method for modulating a biological
XX CC function of an endothelial cell or hematopoietic cell, comprises
XX CC introducing into a cell an antagonist that inhibits binding between a
XX CC PDZ domain protein and a PL domain protein to result in inhibition of
XX CC leukocyte activation. The present sequence is a core sequence of a PL
XX CC domain protein (a T cell surface receptor). PDZ domains of proteins ar-
XX CC named after three prototypical proteins: PSD-95, Drosophila large disc
XX CC protein and Zonula Occludin 1 protein. PDZ domain proteins are involved
XX CC in synapse formation by organising transmembrane neurotransmitter
XX CC receptors through intracellular interactions. The inhibitors identified
XX CC by the present invention can be used to treat a disease mediated by
XX CC hematopoietic cells, e.g. autoimmune disease, inflammation, allergy
XX CC (e.g. drug allergies), inflammatory bowel diseases, ulcerative colitis,
XX CC ileitis, psoriasis, respiratory allergic diseases (e.g. asthma), atopic
XX CC dermatitis, autoimmune diseases (e.g. rheumatoid arthritis, multiple
XX CC sclerosis, insulin-dependent diabetes, Hashimoto thyroiditis,
XX CC osteoarthritis), atherosclerosis, cancers, infectious diseases (e.g.
XX CC viral infection), ischaemia, vasculitis and Crohn's disease. The
XX CC inhibitors can also be used to prevent transplantation rejection of a
XX CC solid organ transplant.
XX SQ Sequence 5 AA:
Query Match 57.1%, Score 4; DB 22; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 KEYF 5
Db ||||
DE 2 KEYF 5
RESULT 8
AAB55783
ID AAB55783 standard; Peptide: 7 AA.
XX AC AAB55783;
XX DT 07-MAR-2001 (first entry)
XX DE PDZ motif sequence #14.
XX KW Hematopoietic cell; PDZ; PL; autoimmune disease; inflammation;
XX KW allergy; asthma; multiple sclerosis; cancer; infection.
XX OS Synthetic.
XX PN W020009896-A2.

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XX PR 23-NOV-2000.
XX PF 12-MAY-2000; 20000S-US13161.
XX PP 14-MAY-1999; 990S-0134114.
XX PP 14-MAY-1999; 990S-0134117.
XX PR 14-MAY-1999; 990S-0134118.
XX PR 21-OCT-1999; 990S-0160860.
XX PR 29-OCT-1999; 990S-0162498.
XX PR 13-DEC-1999; 990S-0170453.
XX PR 14-JAN-2000; 20000S-0176195.
XX PR 14-FEB-2000; 20000S-0182296.
XX PR 11-APR-2000; 20000S-0196460.
XX PR 11-APR-2000; 20000S-0196527.
XX PA (ARBO-) APPROX VITA CORP.
XX PI Lu PS.
XX DR WPI: 2001-061214/07.
XX PT Modulating a biological function of an endothelial cell or
XX PT hematopoietic cell, useful for treating autoimmune diseases and
XX PT infectious diseases, by administering an antagonist that inhibits
XX PT binding between a PDZ protein and a PL protein.
XX PS Disclosure: Page 87-94; 141pp; English.
XX CC The present invention relates to a new method for modulating a
XX CC biological function of an endothelial cell or hematopoietic cell. The
XX CC method involves introducing into a cell, an antagonist that inhibits
XX CC binding between a PDZ protein and a PL protein. The inhibitor is used
XX CC to treat a disease mediated by hematopoietic cells, e.g. autoimmune
XX CC disease. It may also be used to prevent transplantation rejection of
XX CC a solid organ transplant. The method may also be used in the treatment
XX CC of inflammation, allergy, inflammatory bowel diseases, ulcerative
XX CC colitis, ileitis, psoriasis, asthma, atopic dermatitis, autoimmune
XX CC diseases (e.g. rheumatoid arthritis, multiple sclerosis,
XX CC insulin-dependent diabetes, Hashimoto thyroiditis, osteoarthritis,
XX CC graft rejection, transplantation rejection), atherosclerosis, can-
XX CC cers, infectious diseases, ischemia, vasculitis and Crohn's disease.
XX SQ Sequence 7 AA:
Query Match 57.1%, Score 4; DB 22; Length 7;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 KEYF 5
Db ||||
DE 3 KEYF 6
RESULT 9
AAB57615
ID AAB57615 standard; Peptide: 7 AA.
XX AC AAB57615;
XX DT 12-MAR-2001 (first entry)
XX DE Glycophorin C C-terminal core sequence #4.
XX KW Endothelial cell; hematopoietic cell; PDZ domain protein;
XX KW PL domain protein; leukocyte activation; T cell surface receptor;
XX KW synapse formation; transmembrane neurotransmitter receptor;
XX KW autoimmune disease; transplantation rejection; inflammation; allergy;
XX KW inflammatory bowel disease; ulcerative colitis; ileitis; psoriasis;
XX KW asthma; atopic dermatitis; atherosclerosis; cancer; infectious disease;
XX KW ischaemia; vasculitis; Crohn's disease.
XX PN Homo sapiens.

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XX KW W02000069848-A2
 XX KW 23-NOV-2000.
 PD XX
 XX PF 12-MAY-2000: 2000WS-0134114
 PF PR 14-MAY-1999: 940S-0134114.
 PR PR 14-MAY-1999: 940S-0134117.
 PR PR 14-MAY-1999: 940S-0134118.
 PR PR 21-OCT-1999: 940S-0160860.
 PR PR 29-OCT-1999: 940S-0162498.
 PR PR 13-DEC-1999: 940S-0170453.
 PR PR 14-JAN-2000: 2000WS-0176195.
 PR PR 14-FEB-2000: 2000WS-0182296.
 PR PR 11-APR-2000: 2000WS-0194460.
 PR PR 11-APR-2000: 2000WS-0196527.
 XX XX (ARBO-) ARBOR VITA CORP.
 XX PA
 XX Lu PS:
 XX PF WPI: 2001-0250034/03.
 XX PT
 XX PT New inhibitors of binding of a PLZ protein and PLZ protein for
 PT inhibiting T cell-mediated response by hematopoietic cells, or for
 PT treating diseases characterized by inflammatory and humoral immune
 PT responses, e.g. inflammation, cancer.
 XX XX
 XX Disclosure: Page 93; 139pp; English.
 XX XX
 XX CC The present invention relates to a method for modulating a biological
 CC function of an endothelial cell or hematopoietic cell, comprises
 CC introducing into a cell an antagonist that inhibits binding between a
 CC PDZ domain protein and a PL domain protein to result in inhibition of
 CC leukocyte activation. The present sequence is a core sequence of a PL
 CC domain protein (a T cell surface receptor). PDZ domains of proteins are
 CC named after three prototypical proteins: PSD95, Drosophila large disc
 CC protein and zonula occludin 1 protein. PDZ domain proteins are involved
 CC in synapse formation through intracellular interactions. The inhibitors identified
 CC by the present invention can be used to treat a disease mediated by
 CC hematopoietic cells, e.g. autoimmune disease, inflammatory diseases (e.g.
 CC (e.g. drug allergies), inflammatory bowel diseases, ulcerative colitis,
 CC dermatitis, psoriasis, respiratory allergic diseases (e.g. asthma), atopic
 CC osteoarthritis), atherosclerosis, cancers, infectious diseases (e.g.
 CC viral infection), ischaemia, vasculitis and Crohn's disease. The
 CC inhibitors can also be used to prevent transplantation rejection of a
 CC solid organ transplant.
 XX XX
 XX SQ Sequence 7 AA.
 Query Match 57.1%; Score 4; DP 22; Length 7;
 Best Local Similarity 100.0%; Pred. No 7 Re+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 KEVF 5
 DB 3 KEVF 6
 RESULT 10
 AAB58025
 ID AAB58025 standard; Peptide: 7 AA.
 XX AC AAB58025;
 XX DT 12-MAR-2001 (first entry)
 XX DE Glycophorin C C-terminal core sequence #4.
 XX XX

KW Endothelial cell, hematopoietic cell; PDZ domain protein;
 KW PL domain protein; leukocyte activation; T cell surface receptor;
 KW synapse formation; transmembrane neurotransmitter receptor;
 KW autoimmune disease; transplantation rejection; inflammation; allergy;
 KW inflammatory bowel disease; ulcerative colitis; ileitis; proctitis;
 KW asthma; atopic dermatitis; atherosclerosis; cancer; infectious diseases;
 KW ischaemia; vasculitis; Crohn's disease.
 XX OS Homo sapiens.
 XX PN W02000069848-A2.
 XX PD 23-NOV-2000.
 XX PF 12-MAY-2000: 2000WS-0134114.
 PF PR 14-MAY-1999: 940S-0134114.
 PR PR 14-MAY-1999: 940S-0134117.
 PR PR 14-MAY-1999: 940S-0134118.
 PR PR 21-OCT-1999: 940S-0160860.
 PR PR 29-OCT-1999: 940S-0162498.
 PR PR 13-DEC-1999: 940S-0170453.
 PR PR 14-JAN-2000: 2000WS-0176195.
 PR PR 14-FEB-2000: 2000WS-0182296.
 PR PR 11-APR-2000: 2000WS-0194460.
 PR PR 11-APR-2000: 2000WS-0196527.
 XX XX (ARBO-) ARBOR VITA CORP.
 XX PA
 XX Lu PS:
 XX PF WPI: 2001-0251214/07.
 XX PT
 XX PT Modulating a biological function of a hematopoietic cell for treating
 PT an allergic response, or diseases mediated by immune system cells,
 PT comprises introducing into the cell a PDZ-PL interaction enhancer or
 PT inhibitor.
 XX XX
 XX FS Disclosure: Page 96; 143pp; English.
 XX CC The present invention relates to a method for modulating a biological
 CC function of an endothelial cell or hematopoietic cell, comprises
 CC introducing into a cell an antagonist that inhibits binding between a
 CC PDZ domain protein and a PL domain protein to result in inhibition of
 CC leukocyte activation. The present sequence is a core sequence of a PL
 CC domain protein (a T cell surface receptor). PDZ domains of proteins are
 CC named after three prototypical proteins: PSD95, Drosophila large disc
 CC protein and zonula occludin 1 protein. PDZ domain proteins are involved
 CC in synapse formation through intracellular interactions. The inhibitors identified
 CC by the present invention can be used to treat a disease mediated by
 CC hematopoietic cells, e.g. autoimmune disease, inflammatory diseases (e.g.
 CC (e.g. drug allergies), inflammatory bowel diseases, ulcerative colitis,
 CC dermatitis, psoriasis, respiratory allergic diseases (e.g. asthma), atopic
 CC osteoarthritis), atherosclerosis, cancers, infectious diseases (e.g.
 CC viral infection), ischaemia, vasculitis and Crohn's disease. The
 CC inhibitors can also be used to prevent transplantation rejection of a
 CC solid organ transplant.
 XX XX
 XX SQ Sequence 7 AA:
 Query Match 57.1%; Score 4; DP 22; Length 7;
 Best Local Similarity 100.0%; Pred. No 7 Re+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 KEVF 5
 DB 3 KEVF 6
 RESULT 11

AA855784
ID AA855784 standard; Peptide: 8 AA.

XX
AC AA855784;

XX
AC AA855784;

XX
DT 07-MAR-2001 (first entry)

XX
DE PDZ motif sequence #15.

XX
KW Hematopoietic cell; PDZ, PL; autoimmune disease; inflammation; allergy; asthma; multiple sclerosis; cancer; infection.

XX
OS Synthetic.

XX
PN WO200069896-A2.

XX
PD 23-NOV-2000.

XX
PF 12-MAY-2000; 2000WO-US13161.

XX
PR 14-MAY-1999; 9905-0134114.

XX
PR 14-MAY-1999; 9905-0134117.

XX
PR 14-MAY-1999; 9905-0134118.

XX
PR 21-OCT-1999; 9905-0160860.

XX
PR 29-OCT-1999; 9905-0162438.

XX
PR 13-DEC-1999; 9905-0170453.

XX
PR 14-JAN-2000; 2000US-0176156.

XX
PR 14-FEB-2000; 2000US-0182296.

XX
PR 11-APR-2000; 2000US-0182296.

XX
PR 11-APR-2000; 2000US-0196460.

XX
PA (ARBOR) ARBOR VITA CORP.

XX
PI Lu PS;

XX
PI WPI: 2601-080245/09.

XX
XX Modulating a biological function of an endothelial cell.

XX
XX PT Hematopoietic cell; useful for treating autoimmune diseases and

XX
XX PT Infectious diseases; by administering an antagonist that inhibits

XX
XX PT Binding between a PDZ protein and a PL protein

XX
XX PS Disclosure: Page 87-94; 141pp; English.

XX
XX PS The present invention relates to a new method for modulating a

XX
XX CC biological function of an endothelial cell or hematopoietic cell. The

XX
XX CC method involves introducing into a cell an antagonist that inhibits

XX
XX CC binding between a PDZ protein and a PL protein. The inhibitor is used

XX
XX CC to treat a disease mediated by hematopoietic cells, e.g., autoimmune

XX
XX CC disease. It may also be used to prevent transplantation rejection of

XX
XX CC a solid organ transplant. The method may also be used in the treatment

XX
XX CC of inflammation, allergy, inflammatory bowel diseases, ulcerative

XX
XX CC colitis, ileitis, psoriasis, asthma, atopic dermatitis, autoimmune

XX
XX CC diseases (e.g., rheumatoid arthritis, multiple sclerosis,

XX
XX CC insulin-dependent diabetes, Hashimoto thyroiditis, osteoarthritis,

XX
XX CC graft rejection, transplantation rejection), atherosclerosis, cancers,

XX
XX CC infectious diseases, ischemia, vasculitis and Crohn's disease.

XX
SQ Sequence 8 AA;

Query Match

Best Local Similarity 100.0%; Pred. No. 7.8e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Q7 2 KEYF 5

DI 4 KEYF 7

RESULT 12

AA855784

ID AA855784 standard; Peptide: 8 AA.

XX

AC AA857616;

XX
DT 12-MAR-2001 (first entry)

XX
DE Glycophorin C C-terminal core sequence #5.

XX
KW Endothelial cell; hematopoietic cell; PDZ domain protein;

XX
KW synapse formation; leukocyte activation; T cell surface receptor;

XX
KW autoimmune disease; transplantation rejection; inflammation; allergy;

XX
KW inflammatory bowel disease; ulcerative colitis; ileitis; psoriasis;

XX
KW asthma; atopic dermatitis; atherosclerosis; cancer; infectious disease;

XX
KW ischaemia; vasculitis; Crohn's disease.

XX
OS Homo sapiens.

XX
PN WO200069897-A2.

XX
PD 22 NOV 2000.

XX
PF 12-MAY-2000; 2000WO-US13166.

XX
PR 14-MAY-1999; 9905-0134114.

XX
PR 14-MAY-1999; 9905-0134117.

XX
PR 14-MAY-1999; 9905-0134118.

XX
PR 21-OCT-1999; 9905-0160860.

XX
PR 29-OCT-1999; 9905-0162438.

XX
PR 13-DEC-1999; 9905-0176156.

XX
PR 14-JAN-2000; 2000US-0182296.

XX
PR 14-FEB-2000; 2000US-0182296.

XX
PR 11-APR-2000; 2000US-0196460.

XX
PR 11-APR-2000; 2000US-0196527.

XX
PA (ARBOR) ARBOR VITA CORP.

XX
PI Lu PS;

XX
PI WPI: 2601-080245/03.

XX
XX New inhibitors of binding of a PDZ protein and PL protein for

XX
XX PT inhibiting T cell-mediated response by hematopoietic cells or for

XX
XX PT treating diseases characterized by inflammatory and humoral immune

XX
XX PI responses, e.g., inflammation, cancer

XX
XX PS Disclosure: Page 43; 139pp; English.

XX
XX CC The present invention relates to a method for modulating a biological

XX
XX CC function of an endothelial cell or hematopoietic cell. comprises

XX
XX CC introducing into a cell an antagonist that inhibits binding between a

XX
XX CC PDZ domain protein and a PL domain protein to result in inhibition of

XX
XX CC leukocyte activation. The present sequence is a core sequence of a PL

XX
XX CC domain protein, a T cell surface receptor. PDZ domains of proteins are

XX
XX CC named after three prototypical proteins: PTPN22, protein tyrosine phosphatase

XX
XX CC protein and Zonula Occludens-1 protein. PDZ domain proteins are involved

XX
XX CC in synapse formation by organizing transmembrane neurotransmitter

XX
XX CC receptors through intracellular interactions. The inhibitors identified

XX
XX CC by the present invention can be used to treat a disease mediated by

XX
XX CC hematopoietic cells, e.g., autoimmune disease, inflammation, allergy

XX
XX CC (e.g., drug allergies), inflammatory bowel diseases, ulcerative colitis,

XX
XX CC ileitis, psoriasis, respiratory allergic diseases (e.g., asthma), atopic

XX
XX CC dermatitis, autoimmune diseases (e.g., rheumatoid arthritis, multiple

XX
XX CC sclerosis, insulin-dependent diabetes, Hashimoto thyroiditis,

XX
XX CC osteoarthritis), atherosclerosis, cancers, infectious diseases (e.g.,

XX
XX CC viral infection), ischaemia, vasculitis and Crohn's disease. The

XX
XX CC inhibitors can also be used to prevent transplantation rejection of a

XX
XX CC solid organ transplant.

XX
SQ Sequence 8 AA;

Query Match

Best Local Similarity 100.0%; Pred. No. 7.8e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0


```

RESULT 15
AAR97542
ID AAR97542 standard; peptide; 9 AA.
XX
AC AAR97542;
XX
DT 12-FEB-1997 (first entry)
XX
DE Antigenic peptide, corresp to p53 aa 322-330
XX
FW p53; Her-2; Neu; aa; amino acid; CTL; cytotoxic T lymphocyte; target;
KW malignant cell; antigenic; vaccine; immunisation; activation.
XX
OS Homo sapiens.
XX
PN WO9618409-A1.
XX
PD 20-JUN-1996.
XX
PF 14-DEC-1995; 95WO-US16415
XX
PR 14-DEC-1994; 94US-0355558.
XX
PA (SCRI ) SCRIPPS RES INST.
XX
PI Sherman LA;
XX
DR WPI; 1996-300385/30.
XX
PT In vivo activation of tumour-specific cytotoxic T lymphocytes - by
PT contacting with polypeptide(s) derived from human p53 or Her-2/Neu
PT proteins
XX
PS Example 4; Page 94; 158pp; English.
XX
CC AAR97517-897544 are antigenic p53-derived peptides synthesised to be
CC used in an assay for identifying peptides capable of activating
CC cytotoxic T lymphocytes (CTLs) which specifically target malignant
CC cells. CTL-activating peptides can be used in a vaccine for
CC protecting against tumour cell formation. CTLs activated by the
CC peptides will lyse tumour cells displaying specific peptides.
CC Antibodies against CTL-activating peptides are useful for the
CC identification of other similar compounds which may be useful for
CC treating cancer or virally-infected cells. or for diagnosis the
CC peptide and vaccines produced provide immunity to a high percentage
CC of different ethnic groups, i.e. those with different HLA alleles.
XX
SQ Sequence 9 AA
Query Match 57.1%; Score 4; DB 17; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.9e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EYFT 6
Db 5 EYFT 8

Search completed: April 29, 2003, 08:51:54
Job time : 59.9167 secs

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